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Patent
252/123

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Attorney Docket No.: 252/123
 First Named Inventor: James Hoch, et al.
 Prior Application Information:
 Serial No. 09/172,952
 Examiner: Remy Yucel
 Art Unit: 1618

BOX PATENT APPLICATION
 Assistant Commissioner for Patents
 Washington, D. C. 20231

FILING UNDER 37 CFR § 1.53(b)

This is a request for filing for a

☐ continuation ☒ divisional ☐ continuation-in-part (CIP)

application under 37 CFR § 1.53(b) of pending prior application Serial No. 09/172,952 filed on October 14, 1998, by

James Hoch et al., entitled:

METABOLIC SELECTION METHODS

For CONTINUATION or DIVISION APPS only: The entire disclosure of the prior application, from which an oath or declaration is supplied, referenced above, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference. The incorporation can only be relied upon when a portion has been inadvertently omitted from the submitted application parts.

I. APPLICATION ELEMENTS ENCLOSED

89 Page(s) of Written Description
18 Page(s) of Claims
1 Page(s) of Abstract
18 Sheet(s) of Drawings ☐ formal ☒ informal
3 Page(s) of ☐ Declaration or ☒ Declaration and Power of Attorney
☒ Copy from prior application [37 CFR §1.63(d)]
☐ Newly executed
X Other: 34 pgs. sequence listing

CERTIFICATE OF MAILING
 (37 C.F.R. §1.10)

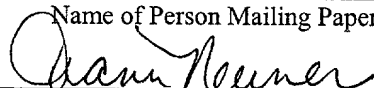
I hereby certify that this paper (along with any referred to as being attached or enclosed) is being deposited with the United States Postal Service on the date shown below with sufficient postage as 'Express Mail Post Office To Addressee' in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

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jc678 U.S. PTO
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- ☒ Assignment papers (cover sheet and documents(s))
- ☒ An Information Disclosure Statement, PTO 1449, ☐ with copies of cited items.
- ☒ A Verified Statement to establish small entity under 37 CFR §§ 1.9 and 1.27: ☐ Is attached. ☒ Has been filed in the prior application and such status is still proper and desired. [37 CFR § 1.28(a)]

II. FEE CALCULATION

BASIC FILING FEE:						\$690.00
Total Claims	23	-	20	=	3	x \$18.00 \$54.00
Independent Claims	3	-	3	=	0	x \$78.00 \$0.00
Multiple Dependent Claims	\$260	(if applicable)			<input type="checkbox"/>	\$0.00
TOTAL OF ABOVE CALCULATIONS						\$744.00
Reduction by ½ for Filing by Small Entity. Note 37 CFR §§ 1.9, 1.27, 1.28. If applicable, Verified Statement must be attached.						<input type="checkbox"/> \$372.00
Misc. Filing Fees (Recordation of Assignment)						\$0.00
TOTAL FEES DUE HEREWITH						\$372.00

III. PRIORITY - 35 USC § 119

- ☐ Priority of application Serial No. _____ filed on _____ in Country is claimed under 35 USC § 119.
- ☐ The certified copy has been filed in prior U.S. application Serial No. _____ on _____.
- ☐ The certified copy will follow.

IV. AMENDMENTS

- ☒ Cancel in this application original Claims 1-71, 95-98 of the prior application before calculating the filing fee. (At least one original independent claim must be retained for filing purposes if no new claims are added in a preliminary amendment.)
- ☐ A Preliminary Amendment is enclosed. (Claims added by Amendment must be numbered consecutively beginning with the number next following the highest numbered original claim in the prior application.)

V. RELATE BACK - 35 USC § 120

- ☐ Relate back information included in preliminary amendment or specification.
- ☒ Please amend the specification as follows:

This application is a division of application serial number 09/172,952, filed October 14, 1998, hereby incorporated by reference herein in totality, including drawings.

- ☐ With respect to the prior co-pending U.S. application from which this application claims benefit under 35 USC § 120, the inventor(s) in this application is (are) [37 CFR 1.53(b)(1)]:
- ☒ the same.
- ☐ less than those named in the prior application and it is requested that the following inventor(s) identified above for the prior application be deleted [see 37 CFR §§1.33(b) AND 1.63(d)(2)]:

[Name(s) of inventor(s) to be deleted]

VI. FEE PAYMENT BEING MADE AT THIS TIME

- ☐ Not attached. No filing fee is submitted. [This and the surcharge required by 37 CFR § 1.16(e) can be paid subsequently.]
- ☒ Attached.

- | | |
|---|-----------------|
| <input checked="" type="checkbox"/> Filing fees. | <u>\$372.00</u> |
| <input type="checkbox"/> Recording assignment. [\$40.00 37 CFR § 1.21(h)(1)] | ----- |
| <input type="checkbox"/> Petition fee for filing by other than all the inventors or person on behalf of the inventor where inventor refused to sign or cannot be reached.
[\$130.00; 37 CFR §§ 1.47 and 1.17(h)] | ----- |
| <input type="checkbox"/> Petition fee to Suspend Prosecution for the Time Necessary to File an Amendment (New Application Filed Concurrently.)
[\$130.00; 37 CFR §§ 1.103 and 1.17(i)] | ----- |
| <input type="checkbox"/> For processing an application with a specification in a non-English language.
[\$130.00; 37 CFR §§ 1.52(d) and 1.17(k)] | ----- |
| <input type="checkbox"/> Processing and retention fee.
[\$130.00; 37 CFR §§ 1.53(f) and 1.21(l)] | ----- |

Total Fees Enclosed \$372.00

VII. METHOD OF PAYMENT OF FEES

- ☒ Attached is a check in the amount of \$372.00.
- ☐ Charge Lyon & Lyon's Deposit Account No. **12-2475** in the amount of _____.

VIII. AUTHORIZATION TO CHARGE ADDITIONAL FEES

The Commissioner is hereby authorized to credit Lyon & Lyon's Deposit Account No. **12-2475** for any over payment of fees and to charge the following additional fees by this paper and during the entire pendency of this application to Deposit Account No. **12-2475**:

- ☒ 37 CFR § 1.16 (Filing fees and excess claims fees)
- ☒ 37 CFR § 1.17 (Application processing fees)
- ☐ 37 CFR § 1.18 (Issue fee at or before mailing of Notice of Allowance, pursuant to 37 CFR § 1.311(b))
- ☒ 37 CFR § 1.21 (Assignment recordation fees)

IX. POWER OF ATTORNEY & CORRESPONDENCE ADDRESS

- ☒ The power appears in the original papers in the prior application.
- ☐ The power does not appear in the original papers, but was filed on _____ in prior application Serial No. _____.
- ☐ A new power has been executed and is attached.

Please send all correspondence to Customer Number 22249:



LYON & LYON LLP
Suite 4700
633 W. Fifth Street
Los Angeles, CA 90071

Please direct all inquiries to Charles S. Berkman, at (858) 626-2602.

X. MAINTENANCE OF CO-PENDENCY OF PRIOR APPLICATION

- ☐ A petition, fee and response has been filed to extend the term in the pending **prior** application until _____. A copy of the petition for extension of time in the **prior** application is attached.
- ☐ A conditional petition for extension of time is being filed in the pending **prior** application. A copy of the conditional petition for extension of time in the **prior** application is attached.


XI. ABANDONMENT OF PRIOR APPLICATION

- ☐ Please abandon the prior application at a time while the prior application is pending or when the petition for extension of time or to revive in that application is granted and when this application is granted a filing date so as to make this application co-pending with said prior application. At the same time, please add the words "now abandoned" to the amendment of the specification set forth in Item V above.

Respectfully submitted,

LYON & LYON LLP

Dated: 9/25/00

By: 
Charles S. Berkman
Reg. No. 38,077

Applicant or Patentee: James Hoch et al.

Serial or Patent No. : 09/172,952

Filed or Issued: October 14, 1998

For: METABOLIC SELECTION METHODS

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS (37 CFR 1.9(f) AND 1.27(c)) – SMALL BUSINESS CONCERN

I hereby declare that I am

- ☐ the owner of the small business concern identified below:
- ☒ an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: MicroGenomics
 ADDRESS OF CONCERN: 11211 Sorrento Valley Road
 San Diego, CA 92121

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under Section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third-part or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled

METABOLIC SELECTION METHODS

by inventor(s) James Hoch and Veronique Dartois

described in

- ☐ the specification filed herewith
- ☒ the application serial no. 09/172,952, filed October 14, 1998.
- ☐ patent no. _____, issued _____.

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below* and no rights to the invention are held by any person, other than the inventor, who could not qualify as an independent inventor under 37 CFR 1.9(c) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

*NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27).

NAME _____

ADDRESS _____

☐ Individual

☐ Small Business Concern

☐ Nonprofit Organization

NAME _____

ADDRESS _____

☐ Individual

☐ Small Business Concern

☐ Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small business entity is no longer appropriate. (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING Veronique Dartois

TITLE OF PERSON SIGNING Senior Scientist

ADDRESS OF PERSON SIGNING 11211 Sorrento Valley Road, San Diego, CA 92121

SIGNATURE *V. Dartois* DATE 04.05.00

DESCRIPTION

METABOLIC SELECTION METHODS

5

FIELD OF THE INVENTION

The present invention relates to methods for screening for enzymatic pathways, and the isolation of the genes and proteins that make up these pathways.

10

BACKGROUND OF THE INVENTION

The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be, or to describe, prior art to the invention.

Biological synthesis of compounds is frequently more cost effective and more productive than chemical synthesis, which can have low yields, require expensive and toxic reagents, and require lengthy purifications. In contrast, biological synthesis using known pathways can be rapid, with high yields. However, the identification of new biological pathways for syntheses of interest is difficult and time consuming.

Currently, the biochemical screening of isolates is a major means by which people find new pathways for the production of chemicals, antibacterials, and other anti-infectives. However, screening is inherently several orders of magnitude slower than selection and requires that the organism be cultured in the laboratory. Since at least 99%

of the microbes in the environment do not grow on laboratory media, less than 1% can be tested using a biochemical screen. Thus, biological pathways in 99% of organisms will never be found by classical biochemical screening technologies.

SUMMARY OF THE INVENTION

The metabolic selection strategy of this invention is designed to find an enzymatic pathway for the conversion of any source compound to any target compound. Conservatively, this technique allows at least a million-fold increase in the discovery rate over classical biochemical screening approaches, and allows testing of the 99% of the environmental microbes that are currently unable to be cultured in the laboratory.

A biocatalytic or metabolic pathway consists of a series of protein catalysts (enzymes) which catalyze the conversion of a starting material to the final product. A general process to identify the metabolic pathway from a source compound to a target compound involves the creation/identification of an easily genetically-manipulatable organism containing an inducible signal, which is activated when a target compound is metabolized. This is followed by the screening of nucleic acid in this organism to identify genes which metabolize the source compound to the target compound.

An example of a selection strategy which can be used to identify the metabolic pathway from a source compound to a target compound is diagrammed in Figure 11. As a first step, microbial isolates are selected that are
5 capable of metabolizing a target compound "T", but not a source compound "S", to an essential factor. Essential factors can include elements like carbon, sulfur, phosphorous, and nitrogen, or other essential nutrients, e.g. some amino acids, fatty acids, and carbohydrates. In a
10 second step, the pathway responsible for the catabolism of compound "T" is identified and made conditional. That is, the gene(s) for the pathway is cloned and placed under control of an inducible promoter such that growth on the target compound is turned "ON" only when the inducer is
15 present. This engineered strain is referred to as the "tester strain". The third part of the strategy is the transfer of foreign DNA from environmental sources into the tester strain, followed by selection for growth on the source compound "S" in the presence of inducer. Such
20 positive clones either are capable of metabolizing compound "S" in the absence of inducer, in which case utilization of "S" does not require prior conversion to compound "T" (Figure 11; pathway I), or alternatively metabolize compound "S" only when "T" catabolism is "ON", suggesting that
25 utilization of "S" proceeds via compound "T" to intermediary metabolism (Figure 11; pathway II). These latter clones are further analyzed and the biocatalysts for the conversion of

"S" to "T" are characterized. A specific embodiment of the metabolic selection strategy is shown in Figure 12, where "S" is 2-keto-L-gulonate (2-KLG), and "T" is ascorbic acid (AsA) which can be metabolized to carbon and energy.

5 Thus, in a first aspect, the invention features a method of screening for one or more nucleic acid sequences which express a product or products that convert a source compound into a target compound. The method comprises contacting a cell with one or more test nucleic acid
10 sequences, where the cell expresses one or more genes encoding one or more proteins which, in the presence of the target compound, provide a detectable signal. The detectable signal indicates the presence of the desired nucleic acid sequence or sequences.

15 The term "screening" as used herein refers to methods for identifying a nucleic acid sequence of interest. Preferably, the method permits the identification of a nucleic acid sequence of interest among one or more sequences, more preferably among hundreds (100, 200, ...900),
20 most preferably among thousands (1,000, 2,000, ...etc.) or more. The sequences to be screened can be isolated from one or more organisms. Preferably, the sequences are isolated from hundreds of organisms, more preferably from thousands or more organisms. The term "screening" may include both
25 classical screening, whereby expression of the nucleic acid results in a phenotype that can be identified (for example by having a colony with the nucleic acid of interest change

color, fluoresce, or luminesce), and may also include classical selection, where typically the phenotype to be identified is growth on selective media. By "selective" is meant media on which the host strain will not grow or grows
5 poorly, but that strains with the nucleic acid of interest will grow in a manner which can be readily distinguished from host strain growth by methods well-known in the art.

The term "nucleic acid" as used herein refers to either deoxyribonucleic acid or ribonucleic acid that may be
10 isolated, enriched, or purified from natural sources or synthesized recombinantly. These methods are well-known in the art and specific examples are also given herein. Preferably, a "nucleic acid" to be identified in the screening method comprises a nucleic acid encoding a
15 metabolic pathway that is not normally found in the cell. Thus, preferably, the pathway has not simply been inactivated through a mutation and the relevant genes are now being identified through complementation. Rather the nucleic acid being identified does not normally exist in the
20 cell in which it is being screened for. Typically, the screening is cross strains, more typically, cross-species, and even more preferably, cross-genera or with further remoteness.

By "isolated, purified, or enriched" in reference
25 to nucleic acid is meant a polymer of 6 (preferably 21, more preferably 39, most preferably 75) or more nucleotides conjugated to each other, including DNA and RNA that is

isolated from a natural source or that is synthesized. In certain embodiments of the invention, longer nucleic acids are preferred, for example those of 300, 600, 900 or more nucleotides and/or those having at least 50%, 60%, 75%, 90%,
5 95% or 99% identity to the sequence shown in SEQ ID NO:1; SEQ ID NO:2; SEQ ID NO:3; SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, or SEQ ID NO:19.

The isolated nucleic acid of the present invention
10 is unique in the sense that it is not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular (i.e., chromosomal) environment. Thus, the sequence may be in a cell-free
15 solution or placed in a different cellular environment. The term does not imply that the sequence is the only nucleotide chain present, but that it is essentially free (about 90-95% pure at least) of non-nucleotide material naturally associated with it, and thus is distinguished from isolated
20 chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the specific DNA or RNA sequence constitutes a significantly higher fraction (2-5 fold) of the total DNA or RNA present in the cells or solution of
25 interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other

DNA or RNA present, or by a preferential increase in the amount of the specific DNA or RNA sequence, or by a combination of the two. However, it should be noted that "enriched" does not imply that there are no other DNA or RNA sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term "significant" is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other nucleic acids of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no DNA or RNA from other sources. The other source DNA may, for example, comprise DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term distinguishes from naturally occurring events, such as viral infection, or tumor type growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least

2-5 fold greater, e.g., in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

The term "expresses a product" as used herein refers to the production of proteins from a nucleic acid vector containing genes within a cell. The nucleic acid vector is transfected into cells using well known techniques in the art as described herein. The "product" may, or may not, be naturally present in the cell.

The term "nucleic acid vector" relates to a single- or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or

independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a desired product can be inserted into a vector by cutting the vector with restriction enzymes and ligating the pieces together, depending on the availability of useful restriction sites. However, there are many methods well-known in the art for the insertion of nucleic acid sequences into vectors.

The term "transfecting" as used herein includes a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "converts" as used herein refers to changing one compound into another compound, preferably enzymatically. The "source compound" refers to the compound to be converted to the "target compound." The "target compound" includes not only the compound that is metabolized to form a detectable signal, but can also include intermediates along the path to a detectable signal. This

is particularly preferred if the target compound is a surrogate target. By "surrogate target compound" is meant a target that is used because the preferable target cannot be used for any of several potential reasons (e.g. if it
5 doesn't cross membranes, has a short half-life, easily broken down, etc.). The "target compound" also includes interconvertible compounds. By "interconvertible" is meant that a pathway exists in the tester strain to convert the compound to the target compound.

10 The term "contacting" as used herein refers to mixing a solution comprising the test nucleic acid with a liquid medium bathing the cells of the methods. The solution comprising the nucleic acid may also comprise other components, such as dimethyl sulfoxide (DMSO), which
15 facilitates the uptake of the test nucleic acid into the cells of the methods. This may also be done by other methods well-known in the art including, but not limited to, transfection or transformation techniques. The solution comprising the test nucleic acid may be added to the medium
20 bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

 The term "cell" as used herein includes the typical definition of a cell, and is further specifically intended to include "cell-free" systems comprising the
25 cellular machinery necessary to express the nucleic acid of the invention. By "cellular machinery" is meant the cellular components present in cell-free transcription

and/or translation systems. Such systems are well-known in the art. In particular, the "cell" lacks the ability to convert a source compound into a target compound, prior to the addition of test nucleic acid sequences. The term

5 "lacks the ability" also includes cells in which the activity may be present but is at too low a level to provide a detectable signal, or is low enough that an additional activity is detectably different. By "detectably different" is meant able to be measured over the background level (e.g.

10 the level of the signal endogenously present in the "cell" and in the equipment used to measure the signal) by an amount greater than the level of error present in the method of measuring.

The term "detectable signal" as used herein refers

15 to a method of identification of the nucleic acids of interest e.g. by color, fluorescence, luminescence or growth.

In preferred embodiments of the method for screening nucleic acid that converts a source compound into

20 a target compound, the one or more nucleic acid sequences encodes a metabolic pathway not normally present in said cell. A "metabolic pathway" consists of a series of protein catalysts (enzymes) which catalyze the conversion of a starting material to a product. And further, by "metabolic

25 pathway" is meant the enzymes, and genes that encode them, that metabolize a source compound to a target compound.

In other preferred embodiments, the nucleic acid is selected from the group consisting of mutagenized DNA, environmental DNA, combinatorial libraries, and recombinant DNA. Preferably, the environmental DNA is selected from the group consisting of mud, soil, sewage, flood control channels, sand, and water. Preferably the mutagenized DNA is the result of enzyme mutagenesis where the mutagenesis is selected from the group consisting of random, chemical, PCR-based, and directed mutagenesis. The directed mutagenesis is to include, for example, DNA shuffling. Preferably the enzymes to be mutagenized in this way are selected from the group consisting of lactonases, esterhydrolases, and reductases.

The term "environmental" as used herein refers to nucleic acids extracted from the environment, e.g. from mud, soil, or water. By "extracted" is meant isolated, enriched, or purified as defined above. The environmental sample can be directly extracted without prior laboratory culture, or can be pre-cultured, for example, in the presence of a growth selective agent. Methods are known in the art and examples are described herein.

In still other preferred embodiments of the method for screening nucleic acid that converts a source compound into a target compound, the detectable signal is selected from a group consisting of growth, fluorescence, luminescence, and color. Methods for detecting these signals are well-known in the art. Preferably, the

detectable signal is growth, and the target compound provides an element or factor required for growth.

Preferably the target compound is selected from the group consisting of ascorbate and 2-keto-L-gulonate (2-KLG), most

5 preferably ascorbate. Preferably the element is selected from the group consisting of carbon, nitrogen, sulfur, and phosphorous. Most preferably, the element is carbon.

Alternatively, the essential factor is another essential nutrient. By "required for growth" is meant that the

10 organism does not grow detectably in the absence of the element. By "provides an element" is meant that the compound can be metabolized by the organism, and that the result of this metabolism is the element in some form, e.g. carbon or carbon dioxide.

15 In other preferred embodiments of the method for screening nucleic acid that converts a source compound into a target compound, the source compound is selected from the group consisting of 2-keto-L-gulonate (2-KLG), 2,5-deoxy-keto-gulonate (2,5-DKG), L-idonate (L-IA), L-gulonate (L-GuA), and glucose, and most preferably 2-KLG.

20

In still other preferred embodiments of the method for screening nucleic acid that converts a source compound into a target compound, the cell naturally expresses the one or more genes encoding one or more proteins that in the presence of the target compound provide a detectable signal. Alternatively, the cell can be genetically manipulated to express the one or more genes encoding one or more proteins that in the presence of the target compound provide a detectable signal. In both cases, the one or more proteins are preferably *Yia* operon-related polypeptides. The one or more genes are preferably under the control of an inducible promoter. The inducible promoter preferably comprises the *trp-lac* hybrid promoter, the *lacO* operator, and the *lacI^r* repressor.

By "naturally expresses" is meant that the genes encoding the proteins are present in the cell in its natural state, e.g. in nature, prior to culture in the laboratory. The genes may or may not be expressed in the natural state, or may or may not be expressed constitutively or inducibly. By "genetically manipulated to express" is meant the transfection of the desired genes into the cell by methods well-known in the art, examples of which are described herein.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different

organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation.

5 Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, ribosome binding site, start codon, and the like. By "inducible promoter" is meant a promoter which is only
10 "on" in the presence of an inducer. The "inducer" is typically a small molecule. Inducible promoters and inducers are well-known in the art and examples are given herein.

The term "Yia operon-related polypeptides" as used
15 herein refers to polypeptides comprising 12 (preferably 15, more preferably 20, most preferably 30) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:10; 31 (preferably 35, more preferably 40, most preferably 50) or more contiguous amino acids set forth in
20 the full-length amino acid sequence of SEQ ID NO:11; 5 (preferably 10, more preferably 15, most preferably 25) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:12, SEQ ID NO:13, or SEQ ID NO:14; 17 (preferably 20, more preferably 25, most
25 preferably 35) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:18; 11 (preferably 15, more preferably

20, most preferably 30) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:16; or a functional derivative thereof as described herein. In certain aspects, polypeptides of 100, 200, 300
5 or more amino acids are preferred. The Yia operon-related polypeptide can be encoded by its corresponding full-length nucleic acid sequence or any portion of its corresponding full-length nucleic acid sequence, so long as a functional activity of the polypeptide is retained (see, Examples
10 section). It is well known in the art that due to the degeneracy of the genetic code numerous different nucleic acid sequences can code for the same amino acid sequence. Equally, it is also well known in the art that conservative changes in amino acid can be made to arrive at a protein or
15 polypeptide which retains the functionality of the original. In both cases, all permutations are within the embodiments of the invention.

The amino acid sequence of the Yia operon-related polypeptide will be substantially similar to the sequence
20 shown in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18, or fragments thereof. A sequence that is substantially similar to the sequence of SEQ ID
NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID
25 NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18 will preferably have at least 90% identity (more preferably at least 95% and most preferably 98-100%) to the

sequence of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18 using a Smith-Waterman protein-protein search.

5 By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues by the total number of residues and gaps and multiplying the product by 100. "Gaps" are spaces in an alignment that are
10 the result of additions or deletions of amino acids. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have deletions, additions, or replacements, may have a lower degree of identity. Those skilled in the art will recognize
15 that several computer programs are available for determining sequence identity. For example, the computer algorithm BLAST is preferably used to search for homologous sequences in a database, and CLUSTAL is used to perform alignments. Identity and similarity determinations can be made using a
20 Smith-Waterman protein-protein search, for example.

 In still other preferred embodiments of the method for screening nucleic acid that converts a source compound into a target compound, the cell grows on ascorbate and does not grow on 2-KLG. Alternatively, the cell may grow on 2-
25 KLG and not grow on 2,5-DKG. Preferably the cells are bacteria. Most preferably, the cell selective for ascorbate is *Klebsiella oxytoca*. By "grows on" is meant that the cell

can utilize the compound (e.g. ascorbate or 2-KLG) as a source of carbon in the minimal essential media. However, the cell is unable to grow in the minimal essential media in the absence of the provided carbon source. Thus, this
5 provides a selective tool for the identification of the nucleic acid encoding the polypeptides of interest.

A second aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding one or more Yia operon-related polypeptides
10 selected from the group consisting of YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS.

In preferred embodiments, the isolated, enriched, or purified nucleic acid molecule encoding one or more Yia operon-related polypeptides comprises a nucleotide sequence
15 that: (a) encodes a polypeptide having the full length amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18; (b) is the complement of the nucleotide sequence of (a); and (c) hybridizes under
20 highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring polypeptide.

In another preferred embodiment, the invention features an isolated, enriched, or purified nucleic acid molecule, wherein said nucleic acid molecule comprises the
25 nucleotide sequence set forth in SEQ ID NO:19. The nucleic acid molecule comprises: (a) one or more nucleotide sequences that are set forth in SEQ ID NO:1, SEQ ID NO:2,

SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9; (b) the complement of the nucleotide sequence of (a); (c) nucleic acid that hybridizes under stringent conditions to the nucleotide molecule of (a); (d) the full length sequence of SEQ ID NO:19, except that it lacks one or more of the sequences set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9; or (e) is the complement of the nucleotide sequence of (d).

10 The term "complement" refers to two nucleotides that can form multiple thermodynamically favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if the nucleotides of the first sequence are complementary to the nucleotides of the second sequence. The percent of complementarity (i.e. how many nucleotides from one strand form multiple thermodynamically favorable interactions with the other strand compared with the total number of nucleotides present in the sequence) indicates the extent of complementarity of two sequences.

25 Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization

conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides.

5 By "stringent hybridization conditions" is meant hybridization conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart's solution at 42 °C overnight; washing
10 with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C.

In other preferred embodiments the isolated, enriched, or purified nucleic acid molecule encoding one or more Yia operon-related polypeptides further comprises a
15 vector or promoter effective to initiate transcription in a host cell. Preferably, the vector or promoter comprises the *trp-lac* hybrid promoter, the *lacO* operator, and the *lacI^s* repressor gene. In still other preferred embodiments, the nucleic acid molecule is isolated, enriched, or purified
20 from a bacteria, preferably *Klebsiella oxytoca*.

The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5,
25 SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9, or a functional derivative thereof, and a vector or a promoter effective to initiate transcription in a host cell. The

recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding one or more Yia operon-related polypeptides and a transcriptional
5 termination region functional in a cell.

In preferred embodiments, the isolated, enriched, purified, recombinant, or recombinant in a cell, nucleic acid comprises, consists essentially of, or consists of the full-length nucleic acid sequence set forth in SEQ ID NO:1,
10 SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9, encodes the full-length amino acid sequence of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18, a
15 functional derivative thereof, or at least 35, 40, 45, 50, 60, 75, 100, 200, or 300 contiguous amino acids of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18. The Yia operon-related polypeptides comprise,
20 consist essentially of, or consist of at least 35, 40, 45, 50, 60, 75, 100, 200, or 300 contiguous amino acids of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18. The nucleic acid may be isolated from a natural
25 source by cDNA cloning or by subtractive hybridization. The natural source may be prokaryotic, eukaryotic, or protozoal, preferably bacterial, from the environment, and the nucleic

acid may be synthesized by the triester method or by using an automated DNA synthesizer. In other preferred embodiments, the nucleic acid molecule is isolated, enriched, or purified from a bacteria, preferably *Klebsiella*
5 *oxytoca*.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the
10 design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a Yia
15 operon-related polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions are provided in Abe, et al. (J. Biol. Chem. 19:13361-13368, 1992), hereby incorporated by reference herein in its
20 entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a Yia operon-
25 related polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 12 (preferably 15, more preferably 20,

most preferably 30) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:10; 30 (preferably 35, more preferably 40, most preferably 50) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:11; 5 (preferably 10, more preferably 15, most preferably 25) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:12, SEQ ID NO:13, or SEQ ID NO:14; 17 (preferably 20, more preferably 25, most preferably 35) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:18; 11 (preferably 15, more preferably 20, most preferably 30) or more contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:16. In particular, a unique nucleic acid region is preferably of bacterial origin.

A third aspect of the invention features a nucleic acid probe for the detection of nucleic acid encoding one or more Yia operon-related polypeptides, selected from the group consisting of YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS, in a sample. Preferably, the nucleic acid probe encodes a polypeptide that is a fragment of the protein encoded by the full length amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18. The nucleic acid probe contains a nucleotide base sequence that will hybridize to the full-

length sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9, or a functional derivative thereof. Hybridization is preferably under stringent
5 conditions.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 12, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID
10 NO:10; at least 30, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:11; at least 5, 12, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of
15 SEQ ID NO:12, SEQ ID NO:13, or SEQ ID NO:14; at least 17, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:18; at least 11, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous
20 amino acids set forth in the full-length amino acid sequence of SEQ ID NO:16, or a functional derivative thereof.

Methods for using the probes include detecting the presence or amount of Yia operon-related RNA in a sample by contacting the sample with a nucleic acid probe under
25 conditions such that hybridization occurs and detecting the presence or amount of the probe bound to Yia operon-related RNA. The nucleic acid duplex formed between the probe and a

nucleic acid sequence coding for a Yia operon-related polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson et al., in Non-isotopic DNA Probe Techniques, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

10 A fourth aspect of the invention features a recombinant cell comprising a nucleic acid molecule encoding one or more Yia operon-related polypeptides selected from the group consisting of YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS. In such cells, the nucleic acid may
15 be under the control of the genomic regulatory elements, or, preferably, may be under the control of exogenous regulatory elements including an exogenous promoter. By "exogenous" is meant a promoter that is not normally coupled *in vivo* transcriptionally to the coding sequence for the Yia operon-related polypeptides.
20

 In preferred embodiments, the recombinant cell comprises nucleic acid encoding a polypeptide that is a fragment of the protein encoded by the amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ
25 ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18. By "fragment," is meant an amino acid sequence present in a Yia operon polypeptide.

Preferably, such a sequence comprises at least 12, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:10; at least 30, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:11; at least 5, 12, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:12, SEQ ID NO:13, or SEQ ID NO:14; at least 17, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:18; at least 11, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:16.

Alternatively, the recombinant cell comprises the nucleic acid sequence set forth in SEQ ID NO:19, or comprises: (a) one or more nucleotide sequences that are set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9; (b) the complement of the nucleotide sequence of (a); (c) nucleic acid that hybridizes under stringent conditions to the nucleotide molecule of (a); (d) the full length sequence of SEQ ID NO:19, except that it lacks one or more of the sequences set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9; and (e) is the complement

of the nucleotide sequence of (d). Preferably, the recombinant cell further comprises a vector or promoter effective to initiate transcription of the above-identified nucleic acid in the cell. Preferably, the vector or
5 promoter comprises the *trp-lac* hybrid promoter, the *lacO* operator, and the *lacI^r* repressor gene. Preferably, the recombinant cell is a bacteria, more preferably *Klebsiella oxytoca*.

Other preferred embodiments of this aspect of the
10 invention include a recombinant cell useful for screening for one or more nucleic acid sequences that express one or more products that convert a source compound into a target compound, where the cell expresses one or more genes, comprising an inducible promoter, and where the one or more
15 genes encodes one or more proteins that in the presence of the target compound and an inducer provide a detectable signal, where the detectable signal indicates the presence of the one or more nucleic acid sequences. Preferably, the detectable signal is selected from a group consisting of
20 growth, fluorescence, luminescence, and color, and most preferably is growth.

In preferred embodiments, of the recombinant cell useful for screening, the one or more nucleic acid sequences encodes a metabolic pathway not normally present in said
25 cell. In other preferred embodiments, the nucleic acid is selected from the group consisting of mutagenized DNA, environmental DNA, combinatorial libraries, and recombinant

DNA. Preferably, the environmental DNA is selected from the group consisting of mud, soil, sewage, flood control channels, sand, and water. Preferably the mutagenized DNA is the result of enzyme mutagenesis where the mutagenesis is selected from the group consisting of random, chemical, PCR-based, and directed mutagenesis. The directed mutagenesis is to include, for example, DNA shuffling. Preferably the enzymes to be mutagenized in this way are selected from the group consisting of lactonases, esterhydrolases, and reductases.

Additionally in this preferred embodiment, the cell preferably requires the presence of the target compound and the inducer for growth. Preferably, the target compound is selected from the group consisting of ascorbate and 2-KLG. In addition, the one or more genes are preferably under the control of an inducible promoter, preferably comprising the *trp-lac* hybrid promoter, the *lacO* operator, and the *lacI^q* repressor gene. Preferably, the one or more proteins encoded by the one or more genes are one or more Yia operon-related polypeptides. Preferably, the cell naturally expresses the one or more genes, or has been genetically manipulated to express the one or more genes. Preferably, the cell is a bacteria, most preferably *Klebsiella oxytoca*.

A fifth aspect of the invention features one or more isolated, enriched, or purified Yia operon-related

polypeptides selected from the group consisting of YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS.

By "isolated" in reference to a polypeptide is meant a polymer of 6 (preferably 12, more preferably 18, most preferably 25, 32, 40, or 50) or more amino acids conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. In certain aspects longer polypeptides are preferred, such as those with 100, 200, 300, 400, or more contiguous amino acids of the sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17 or SEQ ID NO:18.

The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90-95% pure at least) of no-amino acid-based material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2-5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in

the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level this level should be at least 2-5 fold

greater (e.g., in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of
5 substances present in its natural environment at a functionally significant level, for example 90%, 95%, or 99% pure.

In preferred embodiments, the polypeptide is a fragment of the protein encoded by the full length amino
10 acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18. Preferably, the Yia operon polypeptide contains at least 12, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set
15 forth in the full-length amino acid sequence of SEQ ID NO:10; at least 30, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:11; at least 5, 12, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino
20 acids set forth in the full-length amino acid sequence of SEQ ID NO:12, SEQ ID NO:13, or SEQ ID NO:14; at least 17, 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:18; at least 11,
25 32, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids set forth in the full-length amino acid sequence of SEQ ID NO:16, or a functional derivative thereof.

The polypeptide can be isolated from a natural source by methods well-known in the art. The natural source may be protozoal, eukaryotic, or prokaryotic, and the polypeptide may be synthesized using an automated
5 polypeptide synthesizer. Preferably, the polypeptide is isolated, enriched, or purified from bacteria, most preferably *Klebsiella oxytoca*.

In some embodiments the invention includes one or more recombinant Yia operon-related polypeptides. By
10 "recombinant Yia operon-related polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (e.g., present in a different cell or tissue than found in nature), purity or structure. Generally, such
15 a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a sixth aspect, the invention features an antibody (e.g., a monoclonal or polyclonal antibody) having specific binding affinity to a Yia operon-related
20 polypeptide or a Yia operon-related polypeptide fragment. In preferred embodiments, the yia operon-related polypeptide is selected from the group consisting of YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS.

By "specific binding affinity" is meant that the
25 antibody binds to the target Yia operon-related polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody

fragments are polypeptides which contain regions that can bind other polypeptides. The term "specific binding affinity" describes an antibody that binds to a Yia operon polypeptide with greater affinity than it binds to other
5 polypeptides under specified conditions.

The term "polyclonal" refers to antibodies that are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production
10 of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially
15 homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art
20 (Kohler et al., Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term "antibody fragment" refers to a portion
25 of an antibody, often the hypervariable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A

hypervariable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a Yia operon-related polypeptide of the invention may be used in methods for detecting the presence and/or amount of Yia operon polypeptide in a sample by probing the sample with the antibody under conditions suitable for Yia operon-related-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the Yia operon-related polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the Yia operon-related polypeptide as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a Yia operon-related polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a Yia operon-related polypeptide of the invention may be used in methods for detecting the presence and/or amount of Yia

operon-related polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the Yia operon-related polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a seventh aspect, the invention features a hybridoma that produces an antibody having specific binding affinity to a Yia operon-related polypeptide or a Yia operon-related polypeptide fragment. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a Yia operon-related polypeptide of the invention. In preferred embodiments, the antibody to the Yia operon-related polypeptide comprises a sequence of amino acids that is able to specifically bind a Yia operon-related polypeptide of the invention.

In an eighth aspect, the invention features a Yia operon-related polypeptide binding agent able to bind to a Yia operon-related polypeptide. The binding agent is preferably a purified antibody that recognizes an epitope present on a Yia operon-related polypeptide of the invention. Other binding agents include molecules that bind

to Yia operon-related polypeptides and analogous molecules which bind to a Yia operon-related polypeptide. Such binding agents may be identified by using assays that measure Yia operon-related binding partner activity, such as
5 those that measure growth or ascorbate metabolism.

The invention also features a method for screening for other organisms containing a Yia operon-related polypeptide of the invention or an equivalent sequence. The method involves identifying the novel polypeptide in other
10 organisms using techniques that are routine and standard in the art, such as those described herein for identifying the Yia operon-related polypeptide of the invention or others standard in the art (e.g., cloning, Southern or Northern blot analysis, *in situ* hybridization, PCR amplification,
15 etc.).

A ninth aspect of the invention features a method for identifying a substance that converts a source compound to a target compound, comprising: contacting a cell with nucleic acid, where the nucleic acid expresses a product
20 that converts a source compound into a target compound, and where the cell expresses one or more proteins which in the presence of the target compound provide a detectable signal; contacting the cell with a test substance; and monitoring the detectable signal, where the detectable signal indicates
25 the presence of the substance.

In preferred embodiments of the method for identifying a substance that converts a source compound to a

target compound, the substance is selected from the group consisting of antibodies, small organic molecules, peptidomimetics, and natural products. In other preferred embodiments, the detectable signal is selected from a group consisting of growth, fluorescence, luminescence, and color. Preferably, the detectable signal is growth, and the target compound is metabolizable to an element selected from the group consisting of carbon, nitrogen, sulfur, and phosphorous, most preferably carbon. Alternatively, the target compound is metabolizable to an essential nutrient. In still other preferred embodiments of the invention, the source compound is selected from the group consisting of 2-KLG, 2,5-DKG, L-IA, L-GuA, and glucose.

In other highly preferred embodiments of the method for identifying a substance that converts a source compound to a target compound, the one or more proteins are one or more Yia operon-related polypeptides. Preferably, the Yia operon further comprises a vector or promoter effective to initiate transcription in a host cell, and most preferably the vector or promoter comprises the *trp-lac* hybrid promoter, the *lacO* operator, and the *lacI^r* repressor gene.

A tenth aspect of the invention features a method for detecting the presence, absence, or amount of a compound in a sample comprising: contacting the sample with a cell, where the cell expresses one or more genes encoding one or more proteins that in the presence of the compound provide a

detectable signal that indicates the presence, absence, or amount of said compound. A schematic of an example of a preferred embodiment of the method is shown in Fig. 13. In preferred embodiments, the compound is ascorbate and the
5 detectable signal is selected from a group consisting of growth, fluorescence, luminescence, and color. In other preferred embodiments, the one or more genes comprises *yiaJ*, and preferably further comprises a promoter transcriptionally linked to a reporter gene. Preferably,
10 *YiaJ* is naturally expressed in the cell, or the cell has been genetically manipulated to express *YiaJ*. Preferably the reporter gene has a promoter transcriptionally linked and the expression of the reporter gene is regulated by the binding of *YiaJ* to the promoter. The binding of *YiaJ* to the
15 promoter is preferably regulated by the presence or absence of ascorbate. Preferably the cell is a bacteria, and most preferably *Klebsiella oxytoca*.

An eleventh aspect of the invention features an isolated, purified, or enriched nucleic acid molecule
20 encoding *YiaJ* and a reporter gene. Preferably, the nucleic acid molecule further comprises a promoter transcriptionally linked to a reporter gene. Preferably the reporter gene is regulated by the binding of *YiaJ* to the promoter. The binding of *YiaJ* to the promoter is preferably regulated by
25 the presence or absence of ascorbate. In preferred embodiments, the nucleic acid molecule further comprises a

vector or promoter effective to initiate transcription in a host cell.

A twelfth aspect of the invention features a recombinant cell comprising the nucleic acid molecule
5 described in the eleventh aspect of the invention, above.

Preferred embodiments of this aspect of the invention feature a recombinant cell for detecting the presence, absence, or amount of a compound in a sample, where the cell expresses one or more genes encoding one or
10 more proteins that in the presence of the compound provide a detectable signal, where the signal indicates the presence, absence, or amount of the compound. In preferred embodiments, the detectable signal is selected from a group consisting of growth, fluorescence, luminescence, and color.

15 In other preferred embodiments of the recombinant cell for detecting the presence, absence, or amount of a compound in a sample, the one or more genes comprises *yiaJ*, and further comprises a promoter transcriptionally linked to a reporter gene. Preferably, the expression of the reporter
20 gene is regulated by the binding of *YiaJ* to the promoter. Preferably, *yiaJ* is naturally expressed in the recombinant cell, or the cell has been genetically manipulated to express *yiaJ*. The recombinant cell is preferably a bacteria, and more preferably *Klebsiella oxytoca*.

25 A thirteenth aspect of the invention features a method of selection for one or more nucleic acid sequences encoding a metabolic pathway from a source compound to a

target compound comprising: (1) identifying an organism that metabolizes a target compound to provide an essential element; (2) identifying one or more genes responsible for the metabolism of the target compound to the essential
5 element; (3) expressing the one or more genes under the control of an inducible promoter, whereby the target compound is metabolized only in the presence of an inducer and not in the absence of the inducer; (4) expressing nucleic acid sequences potentially encoding the metabolic
10 pathway in the recipient organism; and (5) selecting the recipient organism for growth in the presence of the source compound in the absence of the target compound and in the presence of the inducer, where growth on the source compound in the absence of the target compound and in the presence of
15 the inducer indicates the presence of the nucleic acid sequence.

In preferred embodiments of the method of selection, the essential element is selected from the group consisting of carbon, phosphorous, nitrogen, and sulfur, and most
20 preferably is carbon.

In other preferred embodiments, the method of selection further comprises the transfer of the one or more genes to a highly genetically manipulatable recipient organism, such that the recipient organism metabolizes the target compound
25 to provide an essential element.

By a "highly genetically manipulatable recipient organism" is meant an organism, preferably single-celled,

more preferably bacteria, and most preferably *Klebsiella oxytoca*, that can be manipulated by the standard genetic techniques, including but not limited to, transfection, selection in selective media, growth in culture.

5 The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

10 DESCRIPTION OF THE FIGURES

Figure 1 shows a physical map of the *yiaK-S* operon, which includes the open reading frames *yiaK*, *yiaL*, *orf1*, *yiaX2*, *lyxK*, *yiaQ*, *yiaR*, and *yia*, and its putative regulator, *yiaJ*, compared with the *E. coli yiaK-S* operon, which includes the open reading frames *yiaK*, *yiaL*, *yiaM*, *yiaN*, *yiaO*, *lyxK*, *yiaQ*, *yiaR*, and *yiaS*, and its putative regulator *yiaJ*.

Figures 2A, 2B, 2C, 2D, 2E, and 2F show the nucleic acid sequence (SEQ ID NO:19) and translated amino acid sequences of the open reading frames of the *yia* operon and its putative regulator, *yiaJ*.

Figure 3 shows a multiple sequence alignment of YiaJ-Ko (SEQ ID NO:10), YiaJ-Ec (SEQ ID NO:20), and YiaJ-Hi (SEQ ID NO:21). Identical sequences among the three proteins are indicated by shading.

Figure 4 shows a multiple sequence alignment of YiaK-Ko (SEQ ID NO:11), YiaK-Ec (SEQ ID NO:22), and YiaK-Hi

(SEQ ID NO:23). Identical sequences among the three proteins are indicated by shading.

Figure 5 shows a multiple sequence alignment of YiaJ-Ko (SEQ ID NO:12), YiaL-Ec (SEQ ID NO:24), and YhcH-Hi (SEQ ID NO:25). Identical sequences among the three proteins are indicated by shading.

Figure 6 shows a multiple sequence alignment of LyxK-Ko (SEQ ID NO:15), LyxK-Ec (SEQ ID NO:26), and LyxK-Hi (SEQ ID NO:27). Identical sequences among the three proteins are indicated by shading.

Figure 7 shows a multiple sequence alignment of YiaQ-Ko (SEQ ID NO:16), YiaQ-Ec (SEQ ID NO: 28), and YiaQ-Hi (SEQ ID NO:29). Identical sequences among the three proteins are indicated by shading.

Figure 8 shows a multiple sequence alignment of YiaR-Ko (SEQ ID NO:17), YiaR-Ec (SEQ ID NO:30), and YiaR-Hi (SEQ ID NO:31). Identical sequences among the three proteins are indicated by shading.

Figure 9 shows a multiple sequence alignment of YiaS-Ko (SEQ ID NO:18), YiaS-Ec (SEQ ID NO:32), and YiaS-Hi (SEQ ID NO:33). Identical sequences among the three proteins are indicated by shading.

Figure 10 shows a schematic of the construction of the Tester Strain. The plasmid pMG125 is shown which comprises: (i) a chloramphenicol resistance marker (*cat*); (ii) the thermosensitive origin of replication from plasmid pHO1 (*pHO1 rep (t^s)*); (iii) a 0.8 kb fragment containing the

5' region of the *yiaJ* gene and its promoter sequences; (iv) the spectinomycin resistance marker (*spc*); (v) the *lacI^q*-*lacO-trc* promoter fragment; and (vi) a 1 kb fragment containing the 5' end of *yiaK*, including its ribosome binding site for translation initiation while excluding the promoter sequences of the *yiaK-S* operon. The recombinant plasmid pMG125 was introduced into *K. oxytoca* wild type strain VJSK009 by transformation at 30 °C, the permissive temperature for pMAK705 replication. Chromosomal integration of the pMG125 insert into VJSK009 was achieved by double crossover at the *yiaJ-K* locus such that the endogenous promoter of the *yiaK-S* operon was replaced with the inducible *lacI^q*-*trc* promoter system in the resulting recombinant cell, MGK003.

Figure 11 shows a schematic representation of a general example of a metabolic selection process. Briefly, genetic material, isolated from microbes, is incorporated into a Tester Strain and the gene(s) of interest selected for by growth on "S". The gene(s) of interest will catalyze the conversion of "S" to "T" in the Tester Strain, thereby allowing growth on "S".

Figure 12 shows a schematic representation of a more specific example of metabolic selection process, in which "S" is 2-KLG and "T" is AsA. In this case, the gene(s) of interest are those that catalyze the conversion of 2-KLG to AsA.

Figure 13, part A shows a theoretical model for AsA-dependent activation of the *yiaK-S* operon. Based on transcriptional analyses, the YiaJ regulatory protein is thought to activate transcription of the *yiaK-S* AsA
5 catabolic operon in response to AsA present in the medium. However, the inventors do not wish to be held to this interpretation of the data.

Figure 13, part B shows a schematic representation of a whole-cell reporter system for AsA sensing. The *yiaK-S*
10 promoter region (P_{yia}) is fused to the Green-Fluorescent-Protein (GFP) gene (or to *lux* or other reporter genes), and the fusion is integrated into the chromosome of an indicator strain, which also contains the YiaJ regulator. In the presence of AsA, YiaJ is stimulated and activates
15 transcription of the *yia-GFP* fusion, thereby conferring an easily detectable GFP-positive or fluorescent phenotype.

DETAILED DESCRIPTION OF THE INVENTION

The instant invention is based in part on the use
20 of a metabolic selection strategy that uses a recombinant DNA selection procedure to identify enzymatic pathways for the conversion of a source compound to a target compound. This technique allows at least a million-fold increase in the discovery rate over classical biochemical screening
25 approaches, and allows testing of the 99% of the environmental microbes that are currently not able to be cultured in the laboratory.

The general process involves the creation/
identification of an easily genetically-manipulatable
organism containing an inducible signal, such that the
signal is activated when a target compound is metabolized,
5 followed by the screening of nucleic acid in this organism
to identify genes which metabolize a source compound to the
target compound (Figs. 11 and 12)

In a specific embodiment, the process involves
three steps (1) the identification of an organism capable of
10 metabolizing the target compound to carbon and energy, and
the transfer of this metabolic pathway to a highly
genetically manipulatable organism, e.g. *Escherichia coli* or
Bacillus subtilis, with the result that the recipient now
uses the target compound for growth; (2) placing the
15 expression of the pathway under the control of an inducible
promoter, whereby the target compound is metabolized in the
presence of an inducer and not in its absence; and (3)
cloning genes, which are to be tested for their ability to
metabolize the source compound, into the recipient, and
20 selecting for growth on the source compound in the presence
of the inducer but in the absence of the target compound.

Once positive organisms are identified in the
above selection scheme by growth in the presence of inducer,
the organisms are further screened for their ability to grow
25 in the absence of the inducer. No growth in the absence of
the inducer indicates that the metabolism of the source
compound proceeds via the target compound. Thus, the

nucleic acid probably encodes an enzymatic pathway for the conversion of the source compound to the target compound.

Growth in the absence of the inducer indicates that metabolism of the source compound to the essential
5 element or factor does not require prior conversion to the target compound, rather it may proceed directly, or through an intermediate, to the essential element or factor. When conversion directly to the target compound is the desired result, further work is necessary to obtain the desired
10 genes. methods of obtaining the desired genes include: re-selection of DNA from other sources; random mutation of the DNA followed by re-selection; knocking out (deleting or blocking the expression of genes by methods well-known in the art) the genes that allow the direct conversion to the
15 essential element or factor or from an intermediate to the essential element or factor followed by re-selection; etc. In one preferred embodiment, expression of the genes that allow the direct, or partially direct, conversion to the essential factor are knocked out or their expression
20 blocked, thereby "forcing" the conversion to the essential element through the target compound. This will be effective if a pathway through the target compound existed, but was thermodynamically unfavorable, for example.

Alternatively, if the intermediate is freely
25 interconvertible with the desired target compound as well as to the essential element, growth in the absence of the inducer may be an acceptable outcome, or even desirable. By

"freely interconvertable" is meant that an enzymatic pathway is present to allow the intermediate to be converted to the target. The interconvertability of the compounds would also be determined using the methods described above for

5 obtaining a pathway directly to the target compound.

Under some circumstances, selection of a pathway directly, or through an intermediate, to the essential element or factor rather than to the target compound, is a preferred result. For example, under circumstances where

10 the desired target compound is not one that can be used for direct selection (e.g. does not cross membranes or is rapidly broken down) a "surrogate target" might have to be used. A surrogate target refers to one that is used for selection, but is not the most highly desired target. In

15 this embodiment, the target would preferably be on the pathway of conversion of the surrogate target to the essential element.

I. Functional Derivatives

20 Provided herein are functional derivatives of a polypeptide or nucleic acid of the invention. By "functional derivative" is meant a "chemical derivative," "fragment," or "variant," of the polypeptide or nucleic acid of the invention, which terms are defined below. A

25 functional derivative retains at least a portion of the function of the protein, for example reactivity with an antibody specific for the protein, enzymatic activity or

binding activity mediated through noncatalytic domains,
which permits its utility in accordance with the present
invention. It is well known in the art that due to the
degeneracy of the genetic code numerous different nucleic
5 acid sequences can code for the same amino acid sequence.
Equally, it is also well known in the art that conservative
changes in amino acid can be made to arrive at a protein or
polypeptide which retains the functionality of the original.
In both cases, all permutations are intended to be covered
10 by this disclosure.

Also included with "functional derivatives" of the
polypeptides, in particular, of the invention are "chemical
derivatives". A "chemical derivative" contains additional
chemical moieties not normally a part of the protein.
15 Covalent modifications of the protein or peptides are
included within the scope of this invention. Such
modifications may be introduced into the molecule by
reacting targeted amino acid residues of the peptide with an
organic derivatizing agent that is capable of reacting with
20 selected side chains or terminal residues, for example, as
described below.

Cysteiny l residues most commonly are reacted with
alpha-haloacetates (and corresponding amines), such as
chloroacetic acid or chloroacetamide, to give carboxymethyl
25 or carboxyamidomethyl derivatives. Cysteiny l residues also
are derivatized by reaction with bromotrifluoroacetone,
chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl

disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

Histidyl residues are derivatized by reaction with
5 diethylprocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0.

Lysinyl and amino terminal residues are reacted
10 with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing primary amine containing residues include imidoesters such as methyl picolinimidate; pyridoxal
15 phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginyl residues are modified by reaction with one
20 or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pK_a of the guanidine functional group. Furthermore,
25 these reagents may react with the groups of lysine as well as the arginine alpha-amino group.

Tyrosyl residues are well-known targets of modification for introduction of spectral labels by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizol and tetranitromethane are
5 used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimide ($R'-N-C-N-R'$) such as 1-cyclohexyl-3-(2-morpholinyl(4-ethyl)
10 carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residue are converted to asparaginyl and glutaminyll residues by reaction with ammonium ions.

Glutaminyll and asparaginyl residues are frequently
15 deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

Derivatization with bifunctional agents is useful,
20 for example, for cross-linking the component peptides of the protein to each other or to other proteins in a complex to a water-insoluble support matrix or to other macromolecular carriers. Commonly used cross-linking agents include, for example, 1,1-bis(diazoacetyl)-2-phenylethane,
25 glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-

dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[p-azidophenyl] dithiolpropioimide yield photo-activatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Patent Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains (Creighton, T.E., Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)), acetylation of the N-terminal amine, and, in some instances, amidation of the C-terminal carboxyl groups.

Such derivatized moieties may improve the stability, solubility, absorption, biological half-life, and the like. The moieties may alternatively eliminate or attenuate any undesirable side effect of the protein complex and the like. Moieties capable of mediating such effects are disclosed, for example, in Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA (1990).

The term "fragment" is used to indicate a polypeptide derived from the amino acid sequence of the

proteins, of the complexes having a length less than the full-length polypeptide from which it has been derived. Such a fragment may, for example, be produced by proteolytic cleavage of the full-length protein. Preferably, the

5 fragment is obtained recombinantly by appropriately modifying the DNA sequence encoding the proteins to delete one or more amino acids at one or more sites of the C-terminus, N-terminus, and/or within the native sequence. Fragments of a protein are useful for screening for

10 compounds that act to modulate enzyme activity, as described herein. It is understood that such fragments may retain one or more characterizing portions of the native complex. Examples of such retained characteristics include: catalytic activity; substrate specificity; interaction with other

15 molecules in the intact cell; regulatory functions; or binding with an antibody specific for the native complex, or an epitope thereof.

Another functional derivative intended to be within the scope of the present invention is a "variant"

20 polypeptide which either lacks one or more amino acids or contains additional or substituted amino acids relative to the native polypeptide. The variant may be derived from a naturally occurring complex component by appropriately modifying the protein DNA coding sequence to add, remove,

25 and/or to modify codons for one or more amino acids at one or more sites of the C-terminus, N-terminus, and/or within the native sequence. It is understood that such variants

having added, substituted and/or additional amino acids retain one or more characterizing portions of the native protein, as described above.

A functional derivative of a protein with deleted,
5 inserted and/or substituted amino acid residues may be prepared using standard techniques well-known to those of ordinary skill in the art. For example, the modified components of the functional derivatives may be produced using site-directed mutagenesis techniques (as exemplified
10 by Adelman et al., 1983, DNA 2:183) wherein nucleotides in the DNA coding the sequence are modified, and thereafter expressing this recombinant DNA in a prokaryotic or eukaryotic host cell, using techniques such as those described above. Alternatively, proteins with amino acid
15 deletions, insertions and/or substitutions may be conveniently prepared by direct chemical synthesis, using methods well-known in the art. The functional derivatives of the proteins typically exhibit the same qualitative biological activity as the native proteins.

20

II. Nucleic Acid Probes, Methods, and Kits for Detection of Yia operon-related polypeptides

A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library
25 by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells

according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory, Sambrook, Fritsch, & Maniatis, eds., 1989).

5 In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences which correspond to N-terminal and C-terminal portions of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid
10 probes may be used as primers in a polymerase chain reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press, Michael, et al., eds., 1990, utilizing the appropriate chromosomal or
15 cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art
20 ("Molecular Cloning: A Laboratory Manual", 1989, supra). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After
25 hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples
5 of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in
10 the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary
15 based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample which is compatible with the method
20 utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b)
25 detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art

as described above. Samples to be tested include but should not be limited to RNA samples extracted from environmental samples.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin). Preferably, the kit further comprises instructions for use.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as

phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats which are well known in the art.

III. DNA Constructs Comprising Yia Operon-Related Nucleic Acid Molecules and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells which have been

altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or which the cell
5 normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to
10 be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the
15 regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a
20 promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with
25 initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a Yia operon polypeptide of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a polypeptide of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence encoding a polypeptide of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a polypeptide of the invention, or (3) interfere with the ability of the gene sequence of a polypeptide of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence. Thus, to express a gene encoding a polypeptide of the invention, transcriptional and

translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a polypeptide of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for polypeptides of the invention.

10 Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC18, pUC19 and the like; suitable phage or bacteriophage vectors may include γ gt10, γ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like.

15 Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, *Klebsiella*, and the like. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

25

To express a polypeptide of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the polypeptide of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the α -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ζ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic promoters are reviewed by Glick (Ind. Microbiot. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev.

Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and
5 "cell culture" may be used interchangeably and all such designations include progeny. Thus, the terms "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all
10 progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as long as mutant progeny have the same functionality as that of the originally transformed cell, they are considered to be the same cell or cell-line.

15 Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the polypeptide of interest. Transcriptional initiation regulatory signals may be selected which allow for
20 repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

25 A nucleic acid molecule encoding a polypeptide of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell

either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or a closed covalent circular molecule. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into
5 the host chromosome or as a circular plasmid.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by
10 also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, e.g., antibiotics, or heavy metals, such as copper, or the like. The selectable marker
15 gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters,
20 enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-289, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of
25 autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or

viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector; the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColE1, pSC101, pACYC 184, π VX; "Molecular Cloning: A Laboratory Manual", 1989, supra). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall et al., J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater et al., In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John et al. (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, i.e., transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium

phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned
5 gene(s) results in the production of a polypeptide of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A
10 variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

V. Antibodies, Hybridomas, Methods of Use and Kits for
15 Detection of Yia Operon-Related polypeptides

The present invention relates to an antibody having binding affinity to a polypeptide of the invention. The polypeptide may have the amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,
20 SEQ ID NO:14, SEQ ID NO:10, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, or a functional derivative thereof, or at least 6 contiguous amino acids thereof (preferably, at least 15, 20, 25, 30, 35, or 40 contiguous amino acids thereof).

The present invention also relates to an antibody
25 having specific binding affinity to a polypeptide of the invention. Such an antibody may be isolated by comparing its binding affinity to a polypeptide of the invention with

its binding affinity to other polypeptides. Those which bind selectively to a polypeptide of the invention would be chosen for use in methods requiring a distinction between a polypeptide of the invention and other polypeptides. Such
5 methods could include, but should not be limited to, the identification of other cells expressing the polypeptides of the invention.

The polypeptides of the present invention can be used in a variety of procedures and methods, such as for the
10 generation of antibodies, for use in identifying pharmaceutical compositions, and for selection of other enzymmatic pathways.

The polypeptides of the present invention can be used to produce antibodies or hybridomas. One skilled in
15 the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies.

20 The present invention also relates to a hybridoma which produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

25 In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory

Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St.

Groth et al., J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to

5 produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for
10 immunization will vary based on the animal which is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity.

15 Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

20 For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to
25 identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or

radioimmunoassay (Lutz et al., Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", supra, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, see Stemberger et al., J. Histochem. Cytochem. 18:315, 1970; Bayer et al., Meth. Enzym. 62:308-, 1979; Engval et al., Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues which express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid

supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby et al., Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as immuno-chromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby et al., "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak et al., Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the Yia operon polypeptides of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a Yia operon-related polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that

5 immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Detection of a

10 polypeptide of the invention in a sample may indicate the presence of the pathway of the invention in other cells.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and

15 the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion-based Ouchterlony, or rocket immunofluorescent

20 assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock et al. ("Techniques in

25 Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in

Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane
5 extracts of cells, or environmental samples. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts
10 of cells are well known in the art and can readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit
15 may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. Preferably, the kit also contains instructions for use. In another preferred embodiment, the
20 kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are
25 not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents which

are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats which are well known in the art.

Other methods associated with the invention are described in the examples disclosed herein.

10 EXAMPLES

The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the construction and use of metabolic selection systems, and the isolation of desired enzymatic pathways.

EXAMPLE 1: Construction of a Tester Strain for the Selection of Pathways from 2-KLG to AsA

This example is exemplary of how to construct tester strains, and therefore can be applied to the identification and construction of tester strains for the selection of other metabolic pathways. The basic idea is to take environmental samples and test them for growth on a target compound (in the example, ascorbate). Then, positive colonies are screened for the inability to grow on the source compound (in the example, 2-KLG). The tester strain is the one that grows on the target, but not the source

compound. Once the genes encoding the metabolic pathway for the target compound to the essential factor (an element such as carbon, nitrogen, sulphur or phosphorous, or a nutrient, for example) are identified, they are then place under the control of an inducible promoter, and the tester strain is ready to be utilized to select for the metabolic pathway from the source to the target compound.

If it proves difficult to obtain a tester strain that grows on the target, but not the source, but strains exist that do not grow on the source, then the pathway that permits growth on the target can be isolated and transferred to another strain that doesn't grow on the source in order to obtain the desired tester strain.

Isolation of a Strain that Grows on AsA, but not 2-KLG

Samples from diverse natural environments were collected to use for the isolation of microbes that can utilize ascorbic acid (AsA) as the sole carbon source. No bacterial species has previously been reported to grow on AsA minimal medium.

Environmental samples were collected from freshwater lakes, lemon and orange orchards, residential backyard soils, human and animal solid wastes.

Over 100 microbial isolates, capable of forming visible colonies within 20 hours of incubation at 30 °C on M9 minimal medium containing 0.5% AsA, were selected from these samples. These 100 isolates were then screened for

their ability to grow on 2-Keto-L-Gulonate (2-KLG) minimal medium.

One of the isolates that could utilize AsA as its sole source of carbon and energy, but could not grow on 2-KLG, was identified as *Klebsiella oxytoca* (Table 1). Thus, *Klebsiella oxytoca* was retained as a candidate for genetic engineering of a host strain that can use AsA under controlled conditions for the selection of cloned microbial pathways from 2-KLG to AsA.

Other bacterial strains capable of metabolizing ascorbic acid to carbon and energy were also identified, as were some that also metabolized 2KLG to carbon and energy (Table 1).

TABLE 1

COMPOUND UTILIZATION OF ENVIRONMENTAL ISOLATES

	AsA	2-KLG
<u>GRAM POSITIVES</u>	<u>72 HR</u>	<u>24 HR</u>
<i>Bacillus megaterium</i>	+	+
<i>Streptomyces species</i>	++	++
<i>Yellow Bug</i>	++	+++
<u>GRAM NEGATIVES</u>	<u>24 HR</u>	<u>72 HR</u>
<i>Klebsiella pneumoniae</i>	+++	-
<i>Klebsiella species</i>	+++	-

<i>Klebsiella oxytoca</i>	+++	-
Unknown Malodorous Short Rod	++	-

Identification of Genes Responsible for AsA Catabolism

In order to identify the gene(s) responsible for AsA catabolism in *K. oxytoca*, mutagenesis by transposition insertion was performed in *K. oxytoca* strain VJSK009 (Cali, B. M., et al., 1989. J. Bacteriol. **171**:2666-2672) using the pfd-Tn5 delivery vector as described by Metzger, M., et al., 1992. Nucl. Acids Res. **20**:2265-2270. Among 5,000 clones screened, several mutants that were no longer capable of growing on AsA were identified, most of which were also affected in their ability to grow on conventional carbon sources such as glucose, maltose, pyruvate or succinate. Two of the mutants, however, were specifically affected in AsA utilization and were further characterized by cloning and sequencing the regions adjacent to the transposon insertion.

Characterization of the Genes/Proteins of the Operon

In both mutants, the Tn5 insertion was found to disrupt the same operon of 8 genes. This operon was found to be homologous to the *yiaK-S* operon of *E. coli* (Blattner, F. R., et al., 1997. Science **277**:1453-1462) which is thought to be involved with carbohydrate utilization (Badia, J., et al., 1998. J. Biol. Chem. **273**:8376-8381).

Similarly to *E. coli*, the *K. oxytoca yiaK-S* operon is preceded by a transcriptional regulator, *yiaJ*. A

physical map of the *yiaK-S* operon and its putative regulator is shown in Figure 1. The nucleic acid sequence and translated amino acid sequence of the open reading frames of the operon and its putative regulator are shown in Figure 2

5 A-F.

The functions of the *yia* operon gene products in *K. oxytoca* and *E. coli* are unknown, except for the *E. coli* *lyxK*-encoded enzyme which was shown to phosphorylate L-xylulose and play a key role in the utilization of L-lyxose

10 by *E. coli* (Sanchez, J. C., et al., 1994. J. Biol. Chem. **169**:29665-29669). However, the *yiaK-S* operon is thought to be silent in wild-type *E. coli*, L-xylulose activity could not be detected in wild type cells, and *E. coli* K12 is unable to metabolize L-lyxose (Sanchez, J. C., et al., 1994.

15 *supra*). A similar operon is also present in *Haemophilus influenzae*, but no function has been determined for any of the open reading frames (Fleischmann, R.D., et al., 1995. Science **269**:496-512).

Alignments of the *yia* open reading frames common among the three species are shown (Figs. 3-9). Based on

20 sequence similarities, *yiaQ* has been classified as a putative hexulose-6-phosphate synthase, *yiaR* as a putative hexulose-6-phosphate isomerase, and *yiaS* as a putative sugar isomerase (data not shown).

25

Place Operon under the control of an Inducible Promoter

To engineer *K. oxytoca* as a host strain for the selection of biocatalysts which produce AsA, the promoter of the *yiaK-S* operon was replaced with a DNA fragment that contained the *trp-lac* hybrid promoter of transcription, the *lacO* operator, and the *lacI^q* repressor gene (Brosius, J. 1992. Meth. Enzymol. **216**:469-483). This allows the *yiaK-S* operon, and therefore AsA catabolism, to be turned ON and OFF in a tightly controlled manner in the presence or absence of IPTG, a non-metabolizable inducer of the *lac* promoter. Practically, a 5-way ligation was set up among:

(i) the pMAK705 integration vector which carries a chloramphenicol resistance marker and the thermosensitive origin of replication from plasmid pHO1 (Hamilton, C. M., et al., 1989. J. Bacteriol. **171**:4617-4622); (ii) a 0.8 kb fragment containing the 5' region of the *yiaJ* gene and its promoter sequences; (iii) the spectinomycin resistance marker retrieved from *Staphylococcus aureus* Tn554 (Murphy, E. 1985. Mol. Gen. Genet. **200**:33-39) to follow integration events; (iv) the *lacI^q-lacO-trc* promoter fragment retrieved from pSE380 (InVitrogen, Carlsbad, CA); and (v) a 1 kb fragment containing the 5' end of *yiaK*, including its ribosome binding site for translation initiation while excluding the promoter sequences of the *yiaK-S* operon (Figure 10).

The recombinant plasmid, pMG125, was introduced into *K. oxytoca* wild type strain VJSK009 by transformation at 30 °C, the permissive temperature for pMAK705

replication. Chromosomal integration of the pMG125 insert by double crossover at the *yiaJ-K* locus was achieved by successive temperature switches as described by (Hamilton, C. M., et al., 1989. *supra*). PCR analyses were performed on
5 12 candidates to verify that the endogenous promoter of the *yiaK-S* operon had been replaced with the inducible *lacI^q-trc* promoter system (Figure 10).

The resulting strain, MGK003, proved able to grow on M9 minimal medium supplemented with ASA 0.25% and IPTG 10 to 100 μ M, while no growth was observed on the same medium lacking IPTG.

EXAMPLE 2: Preparation of Environmental DNA Libraries

An example of a currently preferred method for the
15 isolation of DNA from environmental samples is provided below. In the example, purification from soil and water samples are described, however samples can be from any environmental source and the methods adapted according to practices well-known in the art.

20

Direct Isolation of Total DNA from Soil and Water Samples

Total microbial DNA was isolated from various soil and water samples according to the following procedure which is derived and modified from Steffan, R.J., et al., 1988.
25 Appl. Environ. Microbiol. **54**:2908-2915; Whatling, C. A., and C. M. Thomas. 1993. Anal. Biochem. **210**:98-101; and Zhou, J., et al., 1996. Appl. Environ. Microbiol. **62**:316-322.

1. Begin with 100 g wet soil or 50 g dry soil;
150 mL sodium phosphate buffer 0.1 M, pH 4.5;
and 5 g PVPP (acid washed).
2. Blender - medium speed - 3 times for 1 min
(cool down between each cycle).
Add 0.5 mL SDS 20%, blend 5 more seconds.
3. Centrifuge 10 min at 1,000 g at 10 °C.
4. Keep supernatant.
Repeat extraction twice with soil pellet.
5. Combine the 3 supernatants.
Centrifuge 20 min at 10,000 g at 10 °C
6. Wash pellet with cold 0.1% sodium-0.1% sodium
pyrophosphate.
Homogenize with blender for 1 min or shake.
7. Wash pellet with 33 mM Tris-HCl, 1 mM EDTA, pH
8.0.
8. Resuspend in 2 mL 10 mM Tris, pH 7.6; 1 N NaCl.
9. Mix with equal volume 1.2% LMP agarose at 42 °C.
Pour into 1 mL syringes.
Polymerize for 20 min at 4 °C.
10. Incubate 3-4 hours at 37 °C in 20 vol. 1 N NaCl;
100 mM EDTA; 10 mM Tris, pH 7.5; 1% sarkosyl;
1 mg/mL lysozyme.
11. Add 1 mg/mL proteinase K.
Incubate overnight at 45 °C.
12. Wash agarose plugs twice with TE.

Store in 100 mM EDTA; 10 mM Tris at 4 °C.

13. Load noodles on LMP agarose gel 0.7%.

Cut out chromosomal band.

Heat 15 min at 65 °C in TE buffer.

5 Add 2 U GelZyme (InVitrogen) per 200 µL 1%
agarose. Incubate for 2 h at 40 °C.

EtOH precipitate for no more than 30 min at -20
°C.

10 Preparation of Total DNA from Post-Enrichment Cultures

Aliquots from 18 water or soil samples were used
to inoculate 50 mL of M9 minimal medium supplemented with
any one of the following carbon sources: 0.5% 2-KLG; 0.25%
L-idonate (L-IA); 0.25% L-gulonate (L-GuA) and 0.25%

15 ascorbate. Culture flasks were incubated for 2 to 3 days at
30 °C without agitation.

Total DNA was isolated from these cultures as
follows:

1. 20 mL were centrifuged for 5 min at 6,000 rpm.
- 20 2. Pellets were washed with 5 mL Tris 10 mM, EDTA 1
mM pH 8.0 (TE), were centrifuged again, and were resuspended
in 0.9 mL TE.
3. Lysozyme (5 mg/mL) and RNase 100 (µg/mL) were
added, and cells were incubated for 10 min at 37 °C.
- 25 4. Sodium dodecylsulfate (SDS) was added to a final
concentration of 1%, and the tubes were gently shaken until
lysis was completed.

5. 200 mL of a 5 N NaClO₄ stock solution were added to the lysate.

6. The mixture was extracted once with one volume of phenol:chloroform (1:1) and once with one volume of
5 chloroform.

7. Chromosomal DNA was precipitated by adding 2 mL of cold (-20 °C) ethanol and gently coiling the precipitate around a curved Pasteur pipette.

8. DNA was dried for 30 min at room temperature and
10 was resuspended in 100 to 500 µL of Tris 10 mM, EDTA 1 mM, NaCl 50 mM pH 8.0 to obtain a DNA concentration of 0.5 to 1 µg/µL.

EXAMPLE 3: Selection for Nucleic Acid which Converts 2-
15 KLG to AsA (Fig. 12)

This example is exemplary of how to select for nucleic acid sequences that encode metabolic pathways, and therefore can be applied to the identification and selection of sequences encoding other metabolic pathways. Basically,
20 a nucleic acid library is made, according to methods well-known in the art, from nucleic acid sequences isolated from environmental samples (as described in Example 2, for example). This library is then transfected into the tester strain and the resulting pool of transfected cells selected
25 for growth on the source compound (2-KLG in the example) in the absence of the target compound (ascorbate in the example) and the presence of the inducer.

Construction of an Enrichment DNA Library in a Cosmid Vector

The SuperCos1 cosmid vector (Stratagene, La Jolla, CA) is a λ -based cloning system suitable for the cloning of large DNA fragments. After treatment according to the manufacturer's instructions, the 8 kb-long vector appears as two arms flanked by *cos* sites which are recognized by the λ -packaging machinery. Since only DNA molecules from 40 to 48 kb are efficiently packaged in λ -heads, this allows the selective cloning of 32 to 40 kb inserts between the two arms.

Chromosomal DNA extracted from 20 post-enrichment cultures was mixed in equal amounts. Five to ten μ g of the mixture were partially digested with *Sau3A* restriction enzyme to obtain DNA fragments sized between 5 and 50 kb, were dephosphorylated, and were ligated with SuperCos1 arms using conditions recommended by the supplier. One μ g of the ligation mixture was used in an *in vitro* packaging reaction using the Gigapack III Gold packaging kit from Stratagene to create the cosmid library.

Clearly, this procedure can be used to make other chromosomal DNA libraries, for example from other enriched environmental samples, or from chromosomal DNA extracted directly from environmental samples.

Transfection and Selection of the Cosmid Library

Prior to transfection of *K. oxytoca* strain MGK003 with the packaging mixture, the tester strain was transformed with plasmid pCB382 expressing the *E. coli lamB* gene that functions as λ receptor, which appears to be absent or non-functional in most *Klebsiella* strains (De Vries, G. E., et al., 1984. Proc. Natl. Acad. Sci. USA 81:6080-6084). The resulting MGK003 [λ^s] strain was transfected with the packaged products as follows:

10 1. Five mL of liquid LB medium supplemented with 0.2% maltose and 10 mM MgSO_4 were inoculated from an overnight preculture of strain MGK003 [pCB382].

 2. Cells were grown to an OD_{600} of 0.5, were centrifuged at 500 xg for 10 min, and were resuspended in
15 the same volume of 10 mM MgSO_4 .

 3. The packaging products were mixed with 2 mL of cells in 15 mL culture tubes, and were incubated for 20 min at 39 °C without shaking.

 4. After adding 2.5 mL of 2x YT (1% NaCl; 1% yeast
20 extract; 1.6% tryptone), cells were incubated at 37 °C for 1 h under gentle agitation.

 5. A 100 μL -aliquot was plated on LB-kanamycin medium to determine the number of clones present in the cosmid library.

25 6. The remainder was centrifuged at 3000 g for 5 min and was resuspended in 1 mL of M9 minimal medium supplemented with 10 μM IPTG (IPTG concentration can be

varied up to 100 μ M), and aliquots (200 μ L) were plated on M9 plates containing 0.5% 2-KLG and 50 μ M IPTG. 7.

Plates were incubated at 37 °C for 36 h for selecting candidate pathways that would convert 2-KLG to AsA.

5 (Alternatively, selection can be done at 30 °C.)

Among 500,000 clones to which a first selection round was applied, approximately 100 colonies of various sizes appeared on 2-KLG/IPTG plates. These were re-streaked on: (i) LB-kanamycin to verify the presence of the cosmid
10 vector; (ii) 2-KLG/IPTG; and (iii) 2-KLG lacking IPTG to determine if growth of the positive clones on 2-KLG was dependent upon the expression of AsA catabolism.

Two clones were retained that grew on LB-kanamycin and 2-KLG/IPTG, but not on 2-KLG without IPTG within 20 h at
15 37 °C. To verify that the observed phenotype was conferred by the cloned DNA, cosmid DNA was extracted from these two clones and introduced, by electroporation, into strain MGK003. In both cases, the back-cross gave a phenotype identical to that of the original clone obtained in the
20 selection process (Data not shown).

Selection of libraries can also be done on other carbon sources to isolate other pathways, for example on L-gulonate (0.25%) plus IPTG to isolate pathways from L-gulonate to AsA, or on L-idonate (0.25%) plus IPTG to
25 isolate pathways from L-idonate to AsA.

EXAMPLE 4: Isolation of Other Pathways

The metabolic selection strategy described above can also be used for the isolation of other pathways of interest, for example from 2-KLG to L-idonate, or 2-KLG to L-gulonate, or alternatively, to identify new reductase enzymes capable of the conversion of 2,5-DKG to 2-KLG. This conversion is one of the slow steps in the production of ascorbate, so identification of an enzymatic method would be economically useful. Basically, the strategy described in the examples above can be used to isolate any pathway to metabolize a compound as a carbon, nitrogen, sulfur, or potentially, a phosphorous source.

EXAMPLE 5: Directed Evolution of Enzymes

This metabolic selection method is also capable of facilitating the directed evolution of enzymes. One can use this technique to screen known enzymes for mutations leading to higher efficiency, or to better specify optimal temperature or cofactor requirements, in the metabolic utilization of a compound. The mutations can be the result of natural evolution, the result of PCR or chemical mutagenesis, or created through techniques like DNA shuffling.

EXAMPLE 6: Glucose to Ascorbic Acid Directly

Another permutation on this strategy that can be envisioned is to find new pathways for already existing

processes, e.g. selection for a new pathway for the conversion of glucose to ascorbic acid using only a few enzymatic steps. This is feasible using, for example, a strain for which the sequence of the entire genome is known, such as *E. coli* or *B. subtilis*. The genes for the metabolism of glucose can be mutagenized such that the strain can no longer use glucose as a carbon/energy source, and then glucose-utilization pathways can be selected for as described in the previous examples.

EXAMPLE 7: Ascorbate Biosensor (Fig. 13)

As mentioned above, the *yiaJ* protein is thought to be a regulator for the *Yia* operon. The experiments of the invention indicate that the regulatory activity of *YiaJ* may be, in part, modulated by sensing ascorbate. Thus, it is currently believed that the "sensing" of ascorbate by *YiaJ* (perhaps through binding, although the authors do not wish to be restricted to this interpretation) leads to the activation of the *Yia* operon, and thus the use of ascorbate as a carbon/energy source. This potentially results in an extremely sensitive "biosensor" for ascorbate. Thus, for example, it is envisioned that *yiaJ* could be placed in a construct such that when *YiaJ* bound ascorbate a detectable signal resulted, i.e. instead of turning "ON" or "OFF" the *Yia* operon, *YiaJ* could turn "ON" or "OFF" a gene which produces a detectable signal, for example a gene for fluorescence (e.g. β -galactosidase), luminescence (e.g.

luciferase), or color (lac operon, or green fluorescent protein). Methods of constructing these signal constructs are well-known in the art (e.g. Simpson, et al. 1998. TIBTECH 16: 332-338; Applegate, et al. 1998. Applied Environ. Microbiol. 64: 2730-2735; Selifonova and Eaton, 1996. Applied Environ. Microbiol. 62: 778-783).

These biosensor constructs can also be used in the methods of the invention for screening for a metabolic selection pathway instead of using selection on an essential factor or element. In this case, the tester strain would be one that does not have the source to target pathway as determined by the absence of target being detected by the biosensor in the presence or the absence of the source compound. Thus, the biosensor would need to "sense" and to "react to" the presence of the target compound by any one of the methods described above. Following transfection of the library of nucleic acid from environmental sources, the resulting cells would be screened for the presence of the target compound using the biosensor. In order to facilitate the numbers of colonies that would need to be screened, this could be automated read in luminescent or fluorescent readers or sorted by FACS prior to further testing and identification of individual colonies. Although this requires more initial screening than selection using an essential element, this method offers an alternative approach when the appropriate tester strain or the metabolic pathway is not available for screening using an essential

factor. Thus, the biosensor method provides the flexibility to identify pathways for compounds that are not metabolizable to an essential element, factor, or nutrient, but can be any compound for which a "biosensor" can be
5 identified. Biosensors can be identified and created as described above.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as
10 well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein
15 and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made
20 to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

25 The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not

specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions
5 which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are
10 possible within the scope of the invention claimed.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or
15 subgroup of members of the Markush group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

20 Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. A method for screening for one or more nucleic acid sequences that express one or more products that
5 convert a source compound into a target compound, comprising contacting a cell with one or more test nucleic acid sequences, wherein said cell expresses one or more genes encoding one or more proteins that in the presence of said target compound provide a detectable signal, wherein said
10 detectable signal indicates the presence of said one or more nucleic acid sequences.

2. The method of claim 1, wherein said one or more nucleic acid sequences encodes a metabolic pathway not
15 normally present in said cell.

3. The method of claim 2, wherein said one or more nucleic acid sequences are selected from the group consisting of mutagenized DNA, environmental DNA,
20 combinatorial libraries, and recombinant DNA.

4. The method of claim 3, wherein said environmental DNA is isolated from one or more sources selected from the group consisting of mud, soil, water, sewage, flood control
25 channels, and sand.

5. The method of claim 3, wherein said mutagenized DNA is the result of enzyme mutagenesis wherein said mutagenesis is selected from the group consisting of random, chemical, PCR-based, and directed mutagenesis.

5 6. The method of claim 5, wherein said enzyme is selected from the group consisting of lactonases, esterhydrolases, and reductases.

7. The method of claim 1, wherein said detectable
10 signal is selected from a group consisting of growth, fluorescence, luminescence, and color.

8. The method of claim 7, wherein said detectable
15 signal is growth.

9. The method of claim 1, wherein said target compound provides an element required for growth.

10. The method of claim 9, wherein said element is
20 selected from the group consisting of carbon, nitrogen, sulfur, and phosphorous.

11. The method of claim 10, wherein said element is
25 carbon.

12. The method of claim 9, wherein said target compound is selected from the group consisting of ascorbate and 2-KLG.

5 13. The method of claim 12, wherein said target compound is ascorbate.

14. The method of claim 1, wherein said source compound is selected from the group consisting of 2-Keto-L-
10 Gulonate, 2,5-Deoxy-Keto-Gulonate, L-Idonate, L-Gulonate, and glucose.

15 15. The method of claim 14, wherein said source compound is 2-Keto-L-Gulonate.

16. The method of claim 1, wherein said cell naturally expresses said one or more genes encoding said one or more proteins that in the presence of said target compound provide a detectable signal.

20 17. The method of claim 16, wherein said one or more proteins are one or more Yia operon-related polypeptides.

18. The method of claim 1, wherein said cell has been
25 genetically manipulated to express said one or more genes encoding one or more proteins that in the presence of said target compound provide a detectable signal.

19. The method of claim 18, wherein said one or more proteins are one or more Yia operon-related polypeptides.

5 20. The method of claim 18, wherein said one or more genes encoding said one or more proteins are under the control of an inducible promoter.

21. The method of claim 20, wherein said inducible
10 promoter comprises the *trp-lac* hybrid promoter, the *lacO* operator, and the *lacI^q* repressor gene.

22. The method of claim 1, wherein said cell grows on ascorbate and does not grow on 2-Keto-L-Gulonate.
15

23. The method of claim 22, wherein said cell is a bacteria.

24. The method of claim 23, wherein said bacteria is
20 *Klebsiella oxytoca*.

25. The method of claim 1, wherein said cell grows on 2-Keto-L-Gulonate and does not grow on 2,5-Deoxy-Keto-Gulonate.

26. An isolated, enriched, or purified nucleic acid molecule encoding one or more Yia operon-related

polypeptides selected from the group consisting of YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS.

27. The nucleic acid molecule of claim 26, wherein
5 said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide having the full length amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID
10 NO:16, SEQ ID NO:17, or SEQ ID NO:18;

(b) is the complement of the nucleotide sequence of (a); and

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally
15 occurring polypeptide.

28. The nucleic acid molecule of claim 26, further comprising a vector or promoter effective to initiate transcription in a host cell.

20

29. The nucleic acid molecule of claim 26, wherein said nucleic acid molecule is isolated, enriched, or purified from a bacteria.

25 30. The nucleic acid molecule of claim 29, wherein said bacteria is *Klebsiella oxytoca*.

31. A nucleic acid probe for the detection of nucleic acid encoding one or more Yia operon-related polypeptides, selected from the group consisting of YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS, in a sample.

5

32. The probe of claim 31, wherein said polypeptide is a fragment of the protein encoded by the full length amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID
10 NO:16, SEQ ID NO:17, or SEQ ID NO:18.

33. A recombinant cell comprising a nucleic acid molecule encoding one or more Yia operon-related polypeptides selected from the group consisting of YiaJ,
15 YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS.

34. The cell of claim 33, wherein said polypeptide is a fragment of the protein encoded by the amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID
20 NO:17, or SEQ ID NO:18.

35. An isolated, enriched, or purified Yia operon-related polypeptide selected from the group consisting of
25 YiaJ, YiaK, YiaL, ORF1, YiaX2, LyxK, YiaQ, YiaR, and YiaS.

36. The polypeptide of claim 35, wherein said polypeptide is a fragment of the protein encoded by the full length amino acid sequence set forth in SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO:18.

37. The polypeptide of claim 35, wherein said polypeptide is isolated, enriched, or purified from bacteria.

10

38. The nucleic acid molecule of claim 37, wherein said bacteria is *Klebsiella oxytoca*.

39. An isolated, enriched, or purified nucleic acid molecule, wherein said nucleic acid molecule comprises the nucleotide sequence set forth in SEQ ID NO:19.

40. The nucleic acid molecule of claim 39, wherein said nucleic acid molecule comprises:

20 (a) one or more nucleotide sequences that are set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9;

(b) the complement of the nucleotide sequence of (a);

25 (c) nucleic acid that hybridizes under stringent conditions to the nucleotide molecule of (a);

(d) the full length sequence of SEQ ID NO:19,
except that it lacks one or more of the sequences set forth
in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ
ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID
5 NO:9; and

(e) the complement of the nucleotide sequence of
(d).

41. The nucleic acid molecule of either of claims 39
10 or 40, further comprising a vector or promoter effective to
initiate transcription in a host cell.

42. The nucleic acid molecule of claim 41, wherein
said vector or promoter comprises the *trp-lac* hybrid
15 promoter, the *lacO* operator, and the *lacI^r* repressor gene.

43. The nucleic acid molecule of claim 39, wherein
said nucleic acid molecule is isolated, enriched, or
purified from a bacteria.

20

44. The nucleic acid molecule of claim 43, wherein
said bacteria is *Klebsiella oxytoca*.

45. A recombinant cell, comprising the nucleic acid
25 molecule of claim 42.

(d) the full length sequence of SEQ ID NO:19, except that it lacks one or more of the sequences set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, or SEQ ID
5 NO:9; and

(e) the complement of the nucleotide sequence of (d).

41. The nucleic acid molecule of either of claims 39
10 or 40, further comprising a vector or promoter effective to initiate transcription in a host cell.

42. The nucleic acid molecule of claim 41, wherein said vector or promoter comprises the *trp-lac* hybrid
15 promoter, the *lacO* operator, and the *lacI^q* repressor gene.

43. The nucleic acid molecule of claim 39, wherein said nucleic acid molecule is isolated, enriched, or purified from a bacteria.
20

44. The nucleic acid molecule of claim 43, wherein said bacteria is *Klebsiella oxytoca*.

45. A recombinant cell, comprising the nucleic acid
25 molecule of claim 42.

46. A recombinant cell useful for screening for one or more nucleic acid sequences that express one or more products that convert a source compound into a target compound, wherein said cell expresses one or more genes comprising an inducible promoter, and wherein said one or more genes encodes one or more proteins that in the presence of said target compound and an inducer provide a detectable signal, wherein said detectable signal indicates the presence of said one or more nucleic acid sequences.

10

47. The recombinant cell of claim 46, wherein said one or more nucleic acid sequences encodes a metabolic pathway not normally present in said cell.

15

48. The recombinant cell of claim 47, wherein said one or more nucleic acid sequences are selected from the group consisting of mutagenized DNA, environmental DNA, combinatorial libraries, and recombinant DNA.

20

49. The recombinant cell of claim 48, wherein said environmental DNA is isolated from one or more sources selected from the group consisting of mud, soil, water, sewage, flood control channels, and sand.

25

50. The recombinant cell of claim 48, wherein said mutagenized DNA is the result of enzyme mutagenesis wherein

said mutagenesis is selected from the group consisting of random, chemical, PCR-based, and directed mutagenesis.

51. The method of claim 50, wherein said enzyme is
5 selected from the group consisting of lactonases,
esterhydrolases, and reductases.

52. The recombinant cell of claim 46, wherein said
detectable signal is selected from a group consisting of
10 growth, fluorescence, luminescence, and color.

53. The recombinant cell of claim 46, wherein said
detectable signal is growth.

54. The recombinant cell of claim 53, wherein said
15 cell requires the presence of said target compound and said
inducer for growth.

55. The recombinant cell of claim 54, wherein said
20 target compound is selected from the group consisting of
ascorbate and 2-Keto-L-Gulonate.

56. The recombinant cell of claim 46, wherein said one
or more genes are under the control of said inducible
25 promoter.

57. The recombinant cell of claim 56, wherein said inducible promoter comprises the *trp-lac* hybrid promoter, the *lacO* operator, and the *lacI^q* repressor gene.

5 58. The recombinant cell of claim 56, wherein said one or more proteins comprise one or more *Yia* operon-related polypeptides.

59. The recombinant cell of claim 58, wherein said
10 cell naturally expresses said one or more genes.

60. The recombinant cell of claim 58, wherein said
cell has been genetically manipulated to express said one or
more genes.

15 61. The recombinant cell of claim 58, wherein said
cell is a bacteria.

62. The recombinant cell of claim 61, wherein said
20 bacteria is *Klebsiella oxytoca*.

63. A method for identifying a substance that
modulates the conversion of a source compound to a target
compound, comprising:

25 contacting a cell with nucleic acid, wherein said
nucleic acid expresses a product that converts a source
compound into a target compound, and wherein said cell

expresses one or more proteins which in the presence of said target compound provide a detectable signal;

contacting said cell with a test substance; and

monitoring said detectable signal, wherein said

5 detectable signal indicates the presence of said substance.

64. The method of claim 63, wherein the substance is selected from the group consisting of antibodies, small organic molecules, peptidomimetics, and natural products.

10

65. The method of claim 64, wherein said detectable signal is selected from a group consisting of growth, fluorescence, luminescence, and color.

15

66. The method of claim 65, wherein said detectable signal is growth, and wherein said target compound is metabolizable to an element selected from the group consisting of carbon, nitrogen, sulfur, and phosphorous.

20

67. The method of claim 66, wherein said element is carbon.

25

68. The method of claim 63, wherein said source compound is selected from the group consisting of 2-Keto-L-Gulonate, 2,5-Deoxy-Keto-Gulonate, L-Idonate, L-Gulonate, and glucose.

69. The method of claim 63, wherein said one or more proteins are one or more Yia operon-related polypeptides.

70. The method of claim 69, wherein said Yia operon
5 further comprises a vector or promoter effective to initiate transcription in a host cell.

71. The method of claim 70, wherein said vector or promoter comprises the *trp-lac* hybrid promoter, the *lacO*
10 operator, and the *lacI^r* repressor gene.

72. A method for detecting the presence, absence, or amount of a compound in a sample comprising:

contacting said sample with a cell, wherein said cell
15 expresses one or more genes encoding one or more proteins that in the presence of said compound provide a detectable signal that indicates the presence, absence, or amount of said compound.

20 73. The method of claim 72, wherein said compound is ascorbate.

74. The method of claim 72, wherein said detectable
signal is selected from a group consisting of growth,
25 fluorescence, luminescence, and color.

75. The method of claim 72, wherein said one or more genes comprises *yiaJ*.

76. The method of claim 75, wherein said one or more
5 genes further comprises a promoter transcriptionally linked to a reporter gene.

77. The method of claim 76, wherein YiaJ is naturally expressed in said cell.

10

78. The method of claim 76, wherein said cell has been genetically manipulated to express said *yiaJ*.

79. The method of claim 76, wherein the expression of
15 said reporter gene is regulated by the binding of YiaJ to said promoter.

80. The method of claim 72, wherein said cell is a bacteria.

20

81. The method of claim 80, wherein said bacteria is *Klebsiella oxytoca*.

82. An isolated, purified, or enriched nucleic acid
25 molecule encoding YiaJ and a reporter gene.

83. The nucleic acid molecule of claim 82, further comprising a promoter transcriptionally linked to said reporter gene.

5 84. The nucleic acid molecule of claim 83, wherein the expression of said reporter gene is regulated by the binding of YiaJ to said promoter.

10 85. A recombinant cell for detecting the presence, absence, or amount of a compound in a sample comprising the nucleic acid molecule of either of claims 82 or 83.

15 86. A recombinant cell for detecting the presence, absence, or amount of a compound in a sample, wherein said cell expresses one or more genes encoding one or more proteins that in the presence of said compound provide a detectable signal, wherein said signal indicates the presence, absence, or amount of said compound.

20 87. The recombinant cell of claim 86, wherein said detectable signal is selected from a group consisting of growth, fluorescence, luminescence, and color.

25 88. The recombinant cell of claim 86, wherein said one or more genes comprises *yiaJ*.

89. The recombinant cell of claim 88, wherein said one or more genes further comprises a promoter transcriptionally linked to a reporter gene.

5 90. The recombinant cell of claim 89, wherein YiaJ is naturally expressed in said cell.

10 91. The recombinant cell of claim 89, wherein said cell has been genetically manipulated to express said *yiaJ*.

92. The recombinant cell of claim 89, wherein the expression of said reporter gene is regulated by the binding of YiaJ to said promoter.

15 93. The recombinant cell of claim 86, wherein said cell is a bacteria.

94. The recombinant cell of claim 93, wherein said bacteria is *Klebsiella oxytoca*.

20 95. A method of selection for a nucleic acid sequence encoding a metabolic pathway from a source compound to a target compound comprising:

25 (1) identifying an organism that metabolizes a target compound to provide an essential element;

(2) identifying one or more genes responsible for the metabolism of said target compound to said essential element;

5 (3) expressing said one or more genes under the control of an inducible promoter, whereby said target compound is metabolized in the presence of an inducer and not in the absence of said inducer;

(4) expressing nucleic acid sequences potentially encoding said metabolic pathway in said recipient organism;
10 and

(5) selecting said recipient organism for growth on said source compound in the absence of said target compound and in the presence of said inducer, wherein growth on said source compound in the absence of said target compound and
15 in the presence of said inducer indicates the presence of said nucleic acid sequence.

96. The method of claim 95, wherein said essential element is selected from the group consisting of carbon,
20 phosphorous, nitrogen, and sulfur.

97. The method of claim 96, wherein said essential element is carbon.

25 98. The method of claim 95, further comprising the transfer of said one or more genes to a highly genetically manipulatable recipient organism, such that said recipient

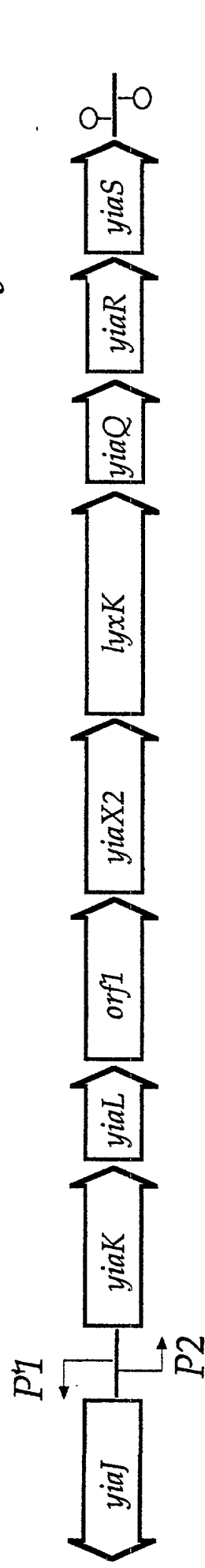
organism metabolizes said target compound to provide an essential element.

ABSTRACT

The present invention relates in part to methods for screening for novel enzymatic pathways in environmental samples using metabolic selection strategies, and the
5 isolation of the genes and proteins that make up these pathways.

Figure 1

Klebsiella oxytoca



Escherichia coli

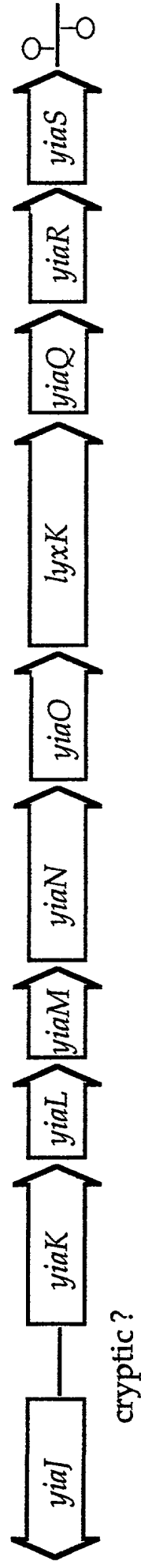


Figure 2A

GGATCCGCGGGCGCAAAGCGGAGACGCCAGAACAGTCCTGGTCTGCTGATGGGACACCACGCAGGCGACTTCACAGGT 80
ACGGCAGCCGATGCACCTTCTCCGCATCCGCGAGAATAAACCGATTTCCTTCTCCATTGGGGATAAAAACGCAGAGTGC 160
CAGAAAAAACCCGCTTTCTCTCCCTTTGATCCTGAATGGAGTCAGCGGCGTTTTCTCTCAGATGTCCGGGATTATCTGG 240

* G E R V S F G L E R S I A E A T D R L P K L
TCATTTGCCTTAACCTTCCCGCACGGAAAAGCCAGTTTCGCGAGAAATCGCCTCTGCCGTATCGCGTAGCGGCTTGAGTA 320

L N K E G V Q K L R S T S L S I S I A Y P V R G H I D
AATTTTCTCTCCACCTGCTTGAGGCGCGATGTTGATAGAGAGATAGAAATGGCATAAGGCACGCGCCCATGGATATCA 400

F V P V A L C S V G L E N E E R D M A M N R E R I Q A
AAAACGGGGACAGCCAGGCACGACACGCCAGCTCGTTCTTCTTCCCTGTCCATCGCCATATTTGCTCGCGGATCTGCGC 480

L E D H M A P L G T I T N R T L P Q I I E Q H S N W
CAGTTCATCATGCATCGCAGGCAAGCCGGTAATGGTATTACGGGTGAGCGCTGGATAATCTCCTGGTGTGAATCCAGT 560

Y S E V Y D P H G F A M Y I K A W Q R A T C R M H Q G
AGCTCTCAACGTAGTCAGGATGGCCAAACGCCATATAAATCtTTGCCATTGCCGAGCAGTACAGCGCATGTGCTGGCCA 640

I Y A R T R L M G T T P E L K Y I L I A H D D E R S S
ATATAGGCGCGGTACGCAGCATACCGTGGTTCGGCTCCAGCTTATAAATCAGGATCGCGTGGTCATCTTCACGGCTGGA 720

F N V T E G T A L N L A E L H P A A V H I I N L S S
GAAGTTCACCGTCTCGCCGGTGGCCAGGTTAAgCGCCTCAAGATGCGGCGCCGCGACGTGGATAATATTCAGCGACGACA 800

L A K Q G V R I F K T T L A Y S G A A P A P T V Y G C
ACGCCCTTTTGCCAACGCGGATAAATTTTGTGCTCAGCGCATAGCTCCCCGCCGCGGGgCAGGCGTCACGTACCCGCGAG 880

S Q L G Q L L R H V T S K N L G A L E S L H A V P C G
GACTGCAGCCCTGTAATAAGCGATGAACGGTACTTTTGTTCAGTCCCGCCAGTTCCGACAGATGCGCCACGGGACAGCC 960

N P Y N S L I E I L M L G R F L S Q S G A P R E K D
ATTGAGATAATTACTCAGGATCTCAATTAGCATCAACCCACGAAAAAGGCTCTGACTTCCGGCAGGCCTCTCTTTATCTT 1040

Q T N E S E K T G M
GCGTGTCTCGCTTTCTTTTGTGCCCATCGCTTCCGCTCCCATTTTTGTGCGGTTTCAGATGGTAGCGCAAAGTGTGTTTC 1120

AGTTCACGATCTGAACCGAAAAACACAACCTTTATGATTTTTATGATTTTTAAAAATAACGCTGCCCGTTGATCTGACAA 1200
AAATTGATCGCTATATTTGAAATCAGATTTTCGCATAGTGAAATTTAGAGATAAAAAAGCGATCAACTCTGACCAGGAAAA 1280

→ *yiaK*
CAGCAATGAAAGTCACGTTTGAGCAGTTAAAGAGGCATTCAATCGGGTACTGCTGGACgcggtgcgtgcgggGGAACCC 1360
M K V T F E Q L K E A F N R V L L D A C V A R E T

GCCGATGCCTGCGCAGAAATGTTTGCCCGCACCACCGAATCCGGCGTCTATTCTCACGGCGTGAACCGCTTCTCTCGCTT 1440
A D A C A E M F A R T T E S G V Y S H G V N R F P R F

CATCCAGCAGTTGGATAACGGCGACATTATCCCTGAGGCTCAACCGCAGCGGGTGACCACGCTCGGCGCCATCGAACAGT 1520
I Q Q L D N G D I I P E A Q P Q R V T T L G A I E Q W

GGGATGCTCAGCGTTCCATCGGCAACCTGACGGCGAAAAAGATGATGGATCGGGCCATTGAGCTGGCCTCCGATCACGGT 1600
D A Q R S I G N L T A K K M M D R A I E L A S D H G

ATCGGCCTGGTGCCTTACGTAATGCTAACCCTGATGCGCGCGCGGCAgTACGGCTGGCAGGCGGCGGAAAAAGGCTA 1680
I G L V A L R N A N H W M R G G S Y G W Q A A E K G Y

CATCGGTATCTGCTGGACCAACTCCATCGCCGTTATGgGCCATGGGGCGCTAAAGAGTGCCGTATCGGTACCAACCCGC 1760
I G I C W T N S I A V M A P W G A K E C R I G T N P L

TGATCGTCCGCTTCCGTCGACGCCGATCACCATGGTGGATATGTCGATGTCGATGTTCTCTACGGCATGCTGGAGGTT 1840
I V A I P S T P I T M V D M S M S M F S Y G M L E V

005349 "9645550

Figure 2B

AACCGCCTTGCCGCGCCGGAAGTGGCGTGGACGGCGGATTGACGATGACGGTCGTTTGACCAAAGAGCCGGGGACGAT 1920
 N R L A G R E L P V D G G F D D D G R L T K E P G T I
 CGAGAAAAATCGCCGCATTTTACCCATGGGCTACTGGAAGGTTCCGGCCTGTCGATCGTCTGGATATGATTGCCACCC 2000
 E K N R R I L P M G Y W K G S G L S I V L D M I A T L
 TCCTCTCAACGGATCGTCGGTTGCCGAAGTGACCCAGGAAAACAGCGATGAATATGGCGTTTCGCAGATCTTCATCGCT 2080
 L S N G S S V A E V T Q E N S D E Y G V S Q I F I A
 ATTGAAGTGGATAAGCTGATCGACGGCGCAACCCGCGACGCCAAGCTGCAACGGATTATGGATTTTCATCACCACCGCCGA 2160
 I E V D K L I D G A T R D A K L Q R I M D F I T T A E
 GCGCGCCGATGAAAATGTGGCGGTCGCTCTTCTGGCCATGAATTTACCCGTCGCTGGATGAAAACCGCCGCAACGGCA 2240
 R A D E N V A V R L P G H E F T R L L D E N R R N G I
 TTACCGTCGATGACAGCGTATGGGCCAAAATTCAGGCGCTGTAAGGAGCTCACCCATGACAGCGTATGGGCCAAAATTC 2320
 T V D D S V W A K I Q A L *
 → *yiaL*
 GCGCTGTAAGGAGCTCACCCATGATTTTGGTCATATTGCTCAACCTAATCCGTGTCGTGCGCCGCGCCATTGAGCG 2400
 M I F G H I A Q P N P C R L P A A I E R
 GCGCTTGATTTCTGCGCACGACGGATTTCCACGCGCTGGCACCCGCGCTCGTGGAAATCGACGGCCAAAACATCTTCG 2480
 A L D F L R T T D F H A L A P G V V E I D G Q N I F A
 CGCAGGTTATCGACTTAACCACTCGCGATGCCGCTGAAAATCGTCCGGAGGTCCACCGTCGCTATCTGGATATCCAGTTT 2560
 Q V I D L T T R D A A E N R P E V H R R Y L D I Q F
 CTGGCATCGGGCGAAgAAAAAATCGGTATCGCCATTGATACCGGCAATAATCAAATCAGCGAATCTTTATTAGAACAGCG 2640
 L A S G E E K I G I A I D T G N N Q I S E S L L E Q R
 CGATATTATTTTTATCACGACAGCGAACATGAATCGTTCTTTGAAATGACGCCAGGCAACTATGCGATATTTTTCCCGC 2720
 D I I F Y H D S E H E S F F E M T P G N Y A I F F P Q
 AAGATGTTTCATCGTCTCGGATGTAATAAACTGTAGCCACGCCGATCCGCAAAATAGTCGTTAAAGTCGCTATTTTCAGTT 2800
 D V H R P G C N K T V A T P I R K I V V K V A I S V
 → *orf1*
 TTATAAGAAGGAGCACAAAATGAATTGAATAATACCGGTTACATTATCGGTGCGTACCCCTGTGCCCCCTGTGCACCCT 2880
 L * M N S N N T G Y I I G A Y P C A P C A P S
 CATTTACCAAAAGAGTGAAGAGGAAGAGaTGAATTTCTGGCGGCAGCTCTCCGACACCCCGGATATTCGCGGGCTGGAG 2960
 F H Q K S E E E E M E F W R Q L S D T P D I R G L E
 CAACCCTGCCTACCCTGCCTTGAACATCTTCATCCGCTCGGCGACGAGTGGTTATTGCGCCATACCCGGGACACTGGCA 3040
 Q P C L P C L E H L H P L G D E W L L R H T P G H W Q
 GATTGTCGTTACCGCCATCATGGAACCATGCGCCGCCGCGGTGAAAACGGCGGCTTTGGGCTGGCGTCCAGCGACGAAA 3120
 I V V T A I M E T M R R R G E N G G F G L A S S D E T
 CGCAGCGCAAAGCCTGCGTGGAGTACTATCGCCACCTGCAGCAGAAGATCGCTAAAATCAATGGCAATACCGCCGGAAA 3200
 Q R K A C V E Y Y R H L Q Q K I A K I N G N T A G K
 GTCATTGCCCTTGAGCTTCACGCCGCCCCGCTGGCGGGCAATGCCAACGTGGCTCAGGCTACCGACGCTTTGCCCGTTC 3280
 V I A L E L H A A P L A G N A N V A Q A T D A F A R S
 ATTAAAGAAATTACCCGCTGGGACTGGTCTGCGAGCTGGTGTGGAGCACTGCGACGCGATGACCGGCAGCGCGCCGC 3360
 L K E I T R W D W S C E L V L E H C D A M T G S A P R
 GCAAAGGATTTTTCGCGTTAGAAAACGTGCTGGAAGCCATTGCCGATTATGACGTTgCATTTGTATTAACTGGGCGCGT 3440
 K G F L P L E N V L E A I A D Y D V G I C I N W A R

005449-967655

Figure 2C

TCGGCCATTGAAGGGCGGAATACCGTGCTACCGCTACCCATACGCAGCAGGTAAAACGGGCAGGAAAGCTCGGCGCGCT 3520
S A I E G R N T V L P L T H T Q Q V K R A G K L G A L

GATgTTTTCTGGCAGCAGCAGgACCGGCGAGTACGGCGAATGGCAGGATTACACGCGCCGTTTCGCGCCTTTCTGCCCGC 3600
M F S G T T Q T G E Y G E W Q D L H A P F A P F C P Q

AgAGCCTGATGACCACCGAACACGCTCGTGAATTATTTGCCTGCGCAGGAACCGCCCCCTGCAATTTTCAGGCATTAAA 3680
S L M T T E H A R E L F A C A G T A P L Q F S G I K

TTACTGGAAATTAATGCCAGCGCAAACGTTGATCATCGCATCGGATATTACGCGACGGCATCTCCGCGCTAAAACAAGC 3760
L L E I N A S A N V D H R I A I L R D G I S A L K Q A

→ *yiaX2*

ACAATAATAATAATCACCTTCATCACCAGAATATTTTAAATATTACGAGACTATAAAGATgAATATAACCTCTAACTCTA 3840
Q * M N I T S N S T

CAACCAAAGATATACCGCGCCAGCGCTGGTTAAGAATCATTCCGCCTATACTGATCACTGTATTATTTCTTATATGGAC 3920
T K D I P R Q R W L R I I P P I L I T C I I S Y M D

CGGGTCAATATTGCCTTTGCGATGCCCCGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCGGGGCTGGCGGG 4000
R V N I A F A M P G G M D A D L G I S A T M A G L A G

CGGTATTTCTTTATCGGTTATCTATTTTACAGGTTCCCGGCGGGAAAATTGCCGTTACGGTAGCGGTAAGAAATTA 4080
G I F F I G Y L F L Q V P G G K I A V H G S G K K F I

TCGGCTGGTTCGCTGGTTCGCTGGGCGGTATCTCCGTGCTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTG 4160
G W S L V A W A V I S V L T G L I T N Q Y Q L L A L

CGCTTCTTACTGGGCGTGGCGGAAGGCGGTATGCTGCCGGTCGTTCTCAGCATGATCAGTAACTGGTTCCTCCCGACGCTGA 4240
R F L L G V A E G G M L P V V L T M I S N W F P D A E

ACGCGGTCGCGCCAACGCGATTGTCTATTATGTTTGTGCCGATTGCCGGGATTATCACCGCCCCACTCTCAGGCTGGATTA 4320
R G R A N A I V I M F V P I A G I I T A P L S G W I I

TCACGGTCTCGACTGGCGCTGGCTGTTTATTATCGAAGGTTTGTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACC 4400
T V L D W R W L F I I E G L L S L V V L V L W A Y T

ATCTATGACCGTCCGCAGGAAGCGCGTGGATTTCCGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTGGCCGCGGAGCA 4480
I Y D R P Q E A R W I S E A E K R Y L V E T L A A E Q

AAAAGCCATTGCCGGCACCGAGGTGAAAAACGCCTCTCTGAGCGCGGTTCTCTCCGACAAAACCATGTGGCAGCTTATCG 4560
K A I A G T E V K N A S L S A V L S D K T M W Q L I A

CCCTGAACTTCTTCTACCAgACCGGCATTTACGGCTACaCCCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGC 4640
L N F F Y Q T G I Y G Y T L W L P T I L K E L T H S

AGCATGGGGCAGGTTCGGCATGCTTGCCATTCTGCCGTACGTTCGGCGCCATTGCTGGGATGTTCTGTTTTCTCCCTTTC 4720
S M G Q V G M L A I L P Y V G A I A G M F L F S S L S

AGACCGAACCGGTAAACGCAAGCTGTTCGTCTGCCTGCCGCTgATTGGCTTCGCTCTGTGCATGTTCTGTCGGTGGCGC 4800
D R T G K R K L F V C L P L I G F A L C M F L S V A L

TgAAAAACCAAATTTGGCTCTCCTATGCCGCGCTGGTTCGGCTGCGGATTCTTCTGCAATCGGCGGCTGGCGTGTCTGG 4880
K N Q I W L S Y A A L V G C G F F L Q S A A G V F W

ACCATCCCGGCACGTCTGTTCAGCGCGGAAATGGCGGGCGGCGCGCGGGGTTATCAACGCGCTTGGCAACCTCGGCGG 4960
T I P A R L F S A E M A G G A R G V I N A L G N L G G

ATTTTGTGGCCCTTATGCCGTCGGGGTGTGATCACGTTgTACAGCAAAGACGCTgGCGTCTATTGCCTGGCGATCTCCC 5040
F C G P Y A V G V L I T L Y S K D A G V Y C L A I S L

Figure 2D

TGGCGCTGGCCGCGCTGATgGCGCTgCTGCTGCCGGCGAAATGCGATGCCgGTGCTGCGCCGGTaAAGACgATAAaTCCA 5120
 A L A A L M A L L L P A K C D A G A A P V K T I N P
 CATAAACGCACTGCGTAAACTCGAGCCCGGCGCGCTgCGCCTGCCGGGCTGCGAAATATGCCGGGTTCACCCGGTaAC 5200
 H K R T A *
 → *lyxK*
 AATgAGATGCgAAAgATGAGCAAgAAACAgGCCTTCTGGCTGGGTATTGATTGCGGCGGCACCTATCTGAAAGCCGGTTT 5280
 M S K K Q A F W L G I D C G G T Y L K A G L
 ATATGACGCCGAAGGTCATGAACATGGCATTGTGCGGCAAGCGCTACGGACGATGTGCCCCCTGCCGGGTACGCCGAAC 5360
 Y D A E G H E H G I V R Q A L R T M S P L P G Y A E R
 GCGACATGCGCCAGCTCTGGCAACACTGCGCGGCGACCATTGCCGGGCTATTACAGCAGGCAGGTGTATCCGGCGAACAG 5440
 D M R Q L W Q H C A A T I A G L L Q Q A G V S G E Q
 ATTAAAGGCGTGGGCATCTCCGCTCAGGGTCAAGGGCTCTTTCTCCTCGATAAGCAGGATCGGCCGCTGGGTAAACGCCAT 5520
 I K G V G I S A Q G Q G L F L L D K Q D R P L G N A I
 CCTCTCCTCCGATCGTCGGGCGCTGAAATCGTTCAGCGCTGGCAGCGGGACCGTATTCCCGAACGGCTCTATCCCGTTA 5600
 L S S D R R A L K I V Q R W Q R D R I P E R L Y P V T
 CCGGCCAGACGCTGTGGACCGGACATCCGGCTTCTTTGCTGCGCTGGGTAAAAGAGAATGAACCCAGCGCTACCGCGAA 5680
 R Q T L W T G H P A S L L R W V K E N E P Q R Y A Q
 ATTGGCTGCGTGATGATGGGGCATGACTATCTGCGCTGGTGCTTAACCGGCGGAAGGGCTGCGAGGAGAGCAACATCTC 5760
 I G C V M M G H D Y L R W C L T G A K G C E E S N I S
 CGAGTCCAACCTCTACAACATGGCCATGGGCCAGTACGACCCGCGCCTGACCGAGTGGCTGGGCATCGGTGAAATCGATA 5840
 E S N L Y N M A M G Q Y D P R L T E W L G I G E I D S
 GCGCGCTGCCCCCGTTGTAGGGTCAGCCGAAATTTGCGGGGAGATCACCGCTCAGGCAGCCGCTTTAACCGGTCTGGCG 5920
 A L P P V V G S A E I C G E I T A Q A A A L T G L A
 GCGGGTACTCCCGTCGTTGGCGGCCTGTTTGACGTGGTCTCCACCGCCCTTTGCGCCGGGATTGAGGATGAGTCGACCCT 6000
 A G T P V V G G L F D V V S T A L C A G I E D E S T L
 CAATGCGGTGATGGGGACCTGGGCCGCTACTAGCGGTATCGCTCACGGCCTGCGCGACCATGAGGCCCACCCCTTACGTCT 6080
 N A V M G T W A V T S G I A H G L R D H E A H P Y V Y
 ATGGCCGCTACGTCAATGACGGCCAGTATATCGTTCACGAAGCCAGCCCGACCTCATCCGGCAACCTcGAATGGTTTACC 6160
 G R Y V N D G Q Y I V H E A S P T S S G N L E W F T
 GCCCAGTGGGGCGATCTCTCGTTTGATGAGATCAATCAGGCCGTCGCCAGCCTGCCGAAAGCCGGGAGCGAGCTGTTTTT 6240
 A Q W G D L S F D E I N Q A V A S L P K A G S E L F F
 TCTGCCGTTTCTGTATGGCAGCAACGCCGGGCTGGAGATGACCTGCGGCTTTTACGGCATGCAGGCGCTGCATACCCGCG 6320
 L P F L Y G S N A G L E M T C G F Y G M Q A L H T R A
 CGCACCTGCTGCAGGCGGTTTATGAAGGCGTGGTATTTAGCCATATGACCCACCTCAGCCGTATGCGCGAACGCTTTACA 6400
 H L L Q A V Y E G V V F S H M T H L S R M R E R F T
 AACGTTCAAGCCCTGCGCGTCACcGGCGGCCCGGCGCACTCCGACGTCTGGATGCAGATGCTGGCGGACGTAAGCGGCTT 6480
 N V Q A L R V T G G P A H S D V W M Q M L A D V S G L
 ACGCATTGAACTCCCGAAGGTGGAAGAGACcGGCTGTTTTGGCGCGGCCCTCGCGCTCGtGTcGGtACcGGCGTATACC 6560
 R I E L P K V E E T G C F G A A L A A R V G T G V Y R
 GCAGcTTTAGCGAAGCCCGGCGCGCCCGGCGAGCACCCGGTGCGCACGcTGCTGCCCGATATGACCGCCACGCGCGCTAT 6640
 S F S E A R R A R Q H P V R T L L P D M T A H A R Y

Figure 2E

→ *yiaQ*

cAGCGCAAATACCGCCACTACcTGCATTGATTGAAGCACTACAGGGCTATCACGCCCGTATTAAGGAGCACGCATTATG 6720
 Q R K Y R H Y L H L I E A L Q G Y H A R I K E H A L *
 M

AGCCGACCATTACTGCAGCTGGCGcTCGACCATAACCAGCCTTCAGGCTGCGCAGCGCGATGTGCCCCTGCTACAGGATCA 6800
 S R P L L Q L A L D H T S L Q A A Q R D V A L L Q D H

CGTTGATATTGTGGAGGCGGGAACCATCCTCTGCTTAACCGAAGGGCTTAGCGCGGTTAAAGCCCTGCGCGCCCAGTGTC 6880
 V D I V E A G T I L C L T E G L S A V K A L R A Q C P

CGGGGAAGATCATCGTCGCCGACTGGAAAGTCGCCGACGCCGGTGAACCCCTGGCGCAGCAGGCCTTTGGCGCTGGCGCC 6960
 G K I I V A D W K V A D A G E T L A Q Q A F G A G A

AACTGGATGACCATCATTTGCGCCGACCCGCTCGCCACGGTCGAGAAAAGGCCACGCGTGGCCCAGGCCTGCGGCGGTGA 7040
 N W M T I I C A A P L A T V E K G H A V A Q A C G G E

AATTCAGATGGAGCTGTTTCGGCAACTGGACGCTGGATGACGCCCCGCGCCTGGTACCGTACCGGCGTCCATCAGGCGATTT 7120
 I Q M E L F G N W T L D D A R A W Y R T G V H Q A I Y

ACCATCGCGGACGCGATGCCCAGGCCAGCGGGCAGCAGTGGGGGGAGGCGGATCTGGCGCGCATGAAAGCGCTGTCCGAT 7200
 H R G R D A Q A S G Q Q W G E A D L A R M K A L S D

ATTGGCCTTGAGCTATCGATTACCGGCGGCATTACCCAGCCGATCTACCGCTGTTCAAAGATATCAACGTCAAAGCCTT 7280
 I G L E L S I T G G I T P A D L P L F K D I N V K A F

TATTGCCGGGCGCGCTGGCAGGCGCGCCCATCCGGCGCGGGTTGCCCGGAATTCCACGCGCAAATCGACGCTATCT 7360
 I A G R A L A G A A H P A R V A A E F H A Q I D A I W

→ *yiaR*

GGGAGAACAGCATGCGTAACCACCCGTTAGGTATTTATGAAAAAGCGCTGGCGAAGGATCTCAGCTGGCCTGAGCGGCT 7440
 G E Q H A *

M R N H P L G I Y E K A L A K D L S W P E R L

GGTACTGGCCAAAAGCTGCGGTTTTGATTTTGTGCGAAATGTGCGTGACGAGACCGATGAACGCCTTTTCGCGCCTGGAGT 7520
 V L A K S C G F D F V E M S V D E T D E R L S R L E W

GGACCCCGGCCAGCGCGCATCGCTGGTGAGCGCGATGCTGGAAACCGGGTCGCCATTCCCTCGATGTGCTTGTCCGCC 7600
 T P A Q R A S L V S A M L E T A V A I P S M C L S A

CATCGCCGTTTTCCCTTTGGCAGCCGCGATGAAGCGGTACGCGATCGGGCGGAGAGATTATGACCAAAGCCATcCGCCT 7680
 H R R F P F G S R D E A V R D R A R E I M T K A I R L

GGCGCGGATCTGGGGATCCGCACCATCCAGCTGGCGGGTTACGACGTCTATTACGAAGAGCATGATGAAGGCACCCGGC 7760
 A R D L G I R T I Q L A G Y D V Y Y E E H D E G T R Q

AGCGTTTTGCGGAAGGGCTGGCCTGGGCGGTAGAACAGGCCGCCCGCGCAGGTAATGCTGGCGGTGGAGATCATGGAC 7840
 R F A E G L A W A V E Q A A A A Q V M L A V E I M D

ACCGCCTTTATGAACTCCATCAGCAAATGAAAAAGTGGGACGAGATGCTTTTCGTACCGTGTTTACCGTCTACCCGGA 7920
 T A F M N S I S K W K K W D E M L S S P W F T V Y P D

CGTCGGCAACCTCAGCGCCTGGGGAAACGACGTACCCGCCGAGCTGAAGCTGGGCATCGATCGTATCGCCGCCATCCACC 8000
 V G N L S A W G N D V T A E L K L G I D R I A A I H L

TGAAAGATACGCTGCCCGTGACCGACGATAGCCCTGGCCAGTTCCGCGACGTGCCGTTTCGgCGAAGGATGCGTCGATTTT 8080
 K D T L P V T D D S P G Q F R D V P F G E G C V D F

GTCGGCATTTTTAAGACGcTGCGCgAGCTGAACTACCGCGGTTTATTTTGATTGAGATGTGGACGGAGAAAGCCAGCGA 8160
 V G I F K T L R E L N Y R G S F L I E M W T E K A S E

→ *yiaS*

003249"0645569

Figure 2F

GCCGGTGCTGGAGATTATCCAGGCCCGGCGCTGGATCGAATCACGGATGCAGGAAGGGGGATTACATGTTAGAACAAC	8240
P V L E I I Q A R R W I E S R M Q E G G F T C *	
M L E Q L	
GAAAGCCGAGGTACTGGCGGCAAACCTGGCCCTCCCCGCACACGGCCTGGTCACCTTTACCTGGGGCAACGTCAGCGCGG	8320
K A E V L A A N L A L P A H G L V T F T W G N V S A V	
TCGATGAAACGCGCAAGCTGATGGTCATTAAGCCCTCCGGCGTCGAATATGAGGTGATGACCGCCGACGATATGGTGGTC	8400
D E T R K L M V I K P S G V E Y E V M T A D D M V V	
GTAGAGATGGCCAGCGGTAAAGTCGTGAAGGCGGTAAAAAACCTCTTCAGATACGCCAACGCATCTGGCGCTTTATCG	8480
V E M A S G K V V E G G K K P S S D T P T H L A L Y R	
CCGCTATCCGCAGATCGGCGGGATCGTGCATACCCACTCCCGCCACGCGACGATCTGGTCGAGGCCGGGCTCGATCTCC	8560
R Y P Q I G G I V H T H S R H A T I W S Q A G L D L P	
CGCCTGGGGCACCACCCACGCGGACTACTTCTATGGCGCGATCCCTGTACCCGACGGATGACCGTTGAGGAGATTAAC	8640
A W G T T H A D Y F Y G A I P C T R R M T V E E I N	
GGCGAGTATGAGTATCAGACCGGCGAGGTGATTATCAAAACCTTTGAACAGCGCGGCCTGGATCCGGCGCAAATCCCGGC	8720
G E Y E Y Q T G E V I I K T F E Q R G L D P A Q I P A	
GGTATTGGTCCATTACACGGCCCCCTTTGCCTGGGGTAAAGACGCCGCCGACGCCGTACATAACGCCGTGGTGCTGGAGG	8800
V L V H S H G P F A W G K D A A D A V H N A V V L E E	
AGTGGCCTACATGGGCCTCTTCTCGCGCCAGTGGCCACAGCTGCCGGATATGCAGTCTGAACTGCTCGATAAACACTAT	8880
C A Y M G L F S R Q W P Q L P D M Q S E L L D K H Y L	
CTGCGTAAACACGGCGCGAACGCTATTACGGGCAAACTAGTCCCGCGGAACCTCCCGGATAAGGCGCTTTGGCCCCCGG	8960
R K H G A N A I T G K T S P A E L P G	
GGGAAGCGTGAGGATGTTGCTGAACTTTCCCGGAGCGATGCTGCGCATCTGTCCGGGCTACGCGTCCCGGCGCTCTGC	9040
GGTCAGCACCGCGCCCGGCGGAAACCCATCAACCCTACGCCGAATTAATATGTCCTTGACGTAACGACGCTTCCACGCC	9120
GCCGGTCCAGGCTGGTGTGCTTGGCGAAAATCTTGCGAAAATAGCCGACATCGTTAAACCCGCATTTTCATCGCCACCTCG	9200
GTAATCGACAGGAATCGCTGATAAGCAGCTTTTCCGCCGCCCTTACCCGCTGACGGTGCAGCGCTTCGGTAACGTCAGC	9280
CGGAAAGCATGGCGATAAACGGCCCCAGATAACCCGCGTTGCAGTGCAGCTCCT	

CGCGTAAACACGGCGCGAACGCTATTACGGGCAAACTAGTCCCGCGGAACCTCCCGGATAAGGCGCTTTGGCCCCCGG

[illegible]

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YiaJ-Ko  KQVGEKNLLK  PLRD TAEA IS  RELGFSVREG  -----
YiaJ-Ec  KQVGEKNLLK  PLRE TAQA IS  NELGFTVRDD  LGA IT
YiaJ-Hi  NKFGTDAFLO  E IRK TAEQ IS  LELGYEN ---  ---- I
```

Figure 4

yiaK-Ko	MKVTFEQLKE	AFNRVLLDAC	VARETADACA	EMFARTTESG	VYSHGVNRFP
yiaK-Ec	MKVTFEQLKA	AFNRV.LISRG	VDSETADACA	EMFARTTESG	VYSHGVNRFP
yiaK-Hi	MRVSYDELKN	EFRV.LLDRO	LTEELAECCA	TAFTD TTQAG	AYSHGINRFP
yiaK-Ko	RFIQQLDNGD	IPEAQPORV	TTLGA IEQWD	AQRS IGNLTA	KKMMDRA IEL
yiaK-Ec	RFIQQLENGD	IIPDAQPKR I	TS LGA IEQWD	AQRS IGNLTA	KKMMDRA IEL
yiaK-Hi	RFIQQLEQGD	IVPNA IPTKV	LS LGS IEQWD	AHQA IGNLTA	KKMMDRA IEL
yiaK-Ko	ASDHG IGLVA	LRNANHWMRG	GSYGWQAAEK	GY IG ICW TNS	IAVMAPWGAK
yiaK-Ec	AADHG IGLVA	LRNANHWMRG	GSYGWQAAEK	GY IG ICW TNS	IAVMPF WGAK
yiaK-Hi	ASQHG VGV IA	LRNANHWMRG	GSYGWQAAEK	GY IG ICW TNA	LAVMPF WGAK
yiaK-Ko	ECR IGTNPLI	VA IPS TP ITM	VDMSMSMFSY	GMLEVNRLAG	RELPVDGGFD
yiaK-Ec	ECR IGTNPLI	VA IPS TP ITM	VDMSMSMFSY	GMLEVNRLAG	RQLPVDGGFD
yiaK-Hi	ECR IGTNPLI	IAPV TTP ITM	VDMSCSMYSY	GMLEVHRLAG	RQTFVDAGFD
yiaK-Ko	DDGRLTKEPG	T IEKNRR ILP	MGYWKGSGLS	IVLDM IATLL	SNGSSVAEVT
yiaK-Ec	DEGNLTKEPG	V IEKNRR ILP	MGYWKGSGMS	IVLDM IATLL	SDGASVAEVT
yiaK-Hi	DEGNL TRDPS	IV EKNRR LLP	MGFWKGSGLS	IVLDM IATLL	SNGESTVAVT
yiaK-Ko	QENSDEYGVIS	Q IF IA IEVDK	L IDGATRDAC	LQR IMDF ITT	AERADENVAV
yiaK-Ec	QDNSDEYGIS	Q IF IA IEVDK	L IDGPTRDAC	LQR IMDYVTS	AERADENQAI
yiaK-Hi	EDKNDEYCVS	QVF IA IEVDR	L IDGKSKDEK	LNR IMDYVKT	AERSDPTQAV
yiaK-Ko	RLPGHEFTRL	LDENRRNG IT	VDDSVWAK IQ	AL	
yiaK-Ec	RLPGHEFTTL	LAENRRNG IT	VDDSVWAK IQ	AL	
yiaK-Hi	RLPGHEFTTI	LSDNQ TNG IP	VDERVWAKLK	TL	

Parameter	Value	Unit
Initial concentration	1.0	mol/L
Temperature	25	°C
Time	0	min
Concentration	1.0	mol/L
Time	10	min
Concentration	0.8	mol/L
Time	20	min
Concentration	0.6	mol/L
Time	30	min
Concentration	0.4	mol/L
Time	40	min
Concentration	0.2	mol/L
Time	50	min
Concentration	0.1	mol/L
Time	60	min
Concentration	0.05	mol/L
Time	70	min
Concentration	0.02	mol/L
Time	80	min
Concentration	0.01	mol/L
Time	90	min
Concentration	0.005	mol/L
Time	100	min
Concentration	0.002	mol/L
Time	110	min
Concentration	0.001	mol/L
Time	120	min
Concentration	0.0005	mol/L
Time	130	min
Concentration	0.0002	mol/L
Time	140	min
Concentration	0.0001	mol/L
Time	150	min
Concentration	0.00005	mol/L
Time	160	min
Concentration	0.00002	mol/L
Time	170	min
Concentration	0.00001	mol/L
Time	180	min
Concentration	0.000005	mol/L
Time	190	min
Concentration	0.000002	mol/L
Time	200	min
Concentration	0.000001	mol/L
Time	210	min
Concentration	0.0000005	mol/L
Time	220	min
Concentration	0.0000002	mol/L
Time	230	min
Concentration	0.0000001	mol/L
Time	240	min
Concentration	0.00000005	mol/L
Time	250	min
Concentration	0.00000002	mol/L
Time	260	min
Concentration	0.00000001	mol/L
Time	270	min
Concentration	0.000000005	mol/L
Time	280	min
Concentration	0.000000002	mol/L
Time	290	min
Concentration	0.000000001	mol/L
Time	300	min
Concentration	0.0000000005	mol/L
Time	310	min
Concentration	0.0000000002	mol/L
Time	320	min
Concentration	0.0000000001	mol/L
Time	330	min
Concentration	0.00000000005	mol/L
Time	340	min
Concentration	0.00000000002	mol/L
Time	350	min
Concentration	0.00000000001	mol/L
Time	360	min
Concentration	0.000000000005	mol/L
Time	370	min
Concentration	0.000000000002	mol/L
Time	380	min
Concentration	0.000000000001	mol/L
Time	390	min
Concentration	0.0000000000005	mol/L
Time	400	min
Concentration	0.0000000000002	mol/L
Time	410	min
Concentration	0.0000000000001	mol/L
Time	420	min
Concentration	0.00000000000005	mol/L
Time	430	min
Concentration	0.00000000000002	mol/L
Time	440	min
Concentration	0.00000000000001	mol/L
Time	450	min
Concentration	0.000000000000005	mol/L
Time	460	min
Concentration	0.000000000000002	mol/L
Time	470	min
Concentration	0.000000000000001	mol/L
Time	480	min
Concentration	0.0000000000000005	mol/L
Time	490	min
Concentration	0.0000000000000002	mol/L
Time	500	min
Concentration	0.0000000000000001	mol/L

yial-Ko VA ISVL-
 yial-Ec VALTALN
 yhcH-Hi VPKV-LI

Figure 6

IyHK-Ko	MSKKQAFWLG	IDCGGTYLKA	GLYDAEGHEH	GIVRQALRTM	SPLPGYAERD
IyHK-Ec	MTQ ---YWLG	LDCGGSWLKA	GLYDREGREA	GVQRLLPLCAL	SPQPGWAERD
IyHK-Hi	MH ---Y YLG	IDCGGTFIKA	AIFDQNGTLO	S IARRN IP II	SEKPGYAERD
IyHK-Ko	MRQLWOHC AA	TIAGLLQQAG	VSGEQIKGVG	ISAQGQGLFL	LDKQDRPLGN
IyHK-Ec	MAELWQCCMA	VIRALLTHSG	VSGEQIVGIG	ISAQKGGLFL	LDKNDKPLGN
IyHK-Hi	MDELWNLC AQ	V IQKT IROSS	ILPQQ IKA IG	ISAQKGGAFF	LDKDNKPLGR
IyHK-Ko	A ILSSDRRAL	K IVQRWORDR	IPERLYPVTR	QTLWTGHPAS	LLRWVKENEP
IyHK-Ec	A ILSSDRRAM	E IVRRWQEDG	IPEKLYPLTR	QTLWTGHPVS	LLRWLKEHEP
IyHK-Hi	A ILSSDQRAY	E IVQCWQKEN	ILOKFYPITL	QTLWMGHPVS	ILRWIKENEP
IyHK-Ko	QRYAQIGCVM	MGHDYLRWCL	TGAKGCEESN	ISESNLYNMA	MGQYDPRLTE
IyHK-Ec	ERYAQIGCVM	MTHDYLRWCL	TGVKGCEESN	ISESNLYNMS	LGEYDPCCLTD
IyHK-Hi	SRYEQIHTIL	MSHDYLRFC L	TEKLYCEETN	ISESNFYNNR	EGKYDIQLAK
IyHK-Ko	WLG IGE IDSA	LPPVVGSAE I	CGE ITAQAAA	LTGLAAGTPV	VGGLEDVVS T
IyHK-Ec	WLG IAE INHA	LPPVVGSAE I	CGE ITAQ TAA	LTGLKAGTPV	VGGLEDVVS T
IyHK-Hi	LFG ITEC IDK	LPP I IKSNT	AGYVTSRAAE	QSGLVEG IPV	VGGLEDVVS T
IyHK-Ko	ALCAG IEDES	TINAVMGTTWA	VTSG IAHGLR	DHEAHPYVYG	RYVNDGQY IV
IyHK-Ec	ALCAG IEDEF	TINAVMGTTWA	VTSG ITRGLR	DGEAHPYVYG	RYVNDGEF IV
IyHK-Hi	ALCADLKDDQ	HLNVVLGTWS	VVSGVTHY ID	DNQTIFFVYG	KYPEKNKFII
IyHK-Ko	HEASPTSSGN	LEWFTAQWGD	LSFDE INQAV	ASLPKAGSEL	FFLPFLYGSN
IyHK-Ec	HEASPTSSGN	LEWFTAQWGE	ISFDE INQAV	ASLPKAGGDL	FFLPFLYGSN
IyHK-Hi	HEASPTSAGN	LEWFVNQFNL	PNYDD INHE I	AKLKPASSSV	LFAPFLYGSN
IyHK-Ko	AGLEMTSGFY	GMQALHTRAH	LLQAVYEGVV	FSHMTHL SRM	RERFTNVQAL
IyHK-Ec	AGLEMTSGFY	GMQA IHTRAH	LLQA IYEGVV	FSHMTHLNRM	RERFTDVHTL
IyHK-Hi	AKLGMQAGFY	G IQSHHTQ IH	LLQA IYEGV I	FSLMSHLERM	QVRFPNASTV
IyHK-Ko	RV TGGPAHSD	VWMQMLADVS	GLR IELPKVE	ETGCFGAA LA	ARVGTGVYRS
IyHK-Ec	RV TGGPAHSD	VWMQMLADVS	GLR IELPOVE	ETGCFGAA LA	ARVGTGVYHN
IyHK-Hi	RV TGGPAKSE	VWMQMLAD IS	GMRLE IPN IE	ETGCLGAALM	AMQAESA ---
IyHK-Ko	FSEBARRARQH	PVRTLLPDMT	AHARYQRKYR	HYLHL IEALQ	GYHAR IKEHA
IyHK-Ec	FSEAQRDLRH	PVRTLLPDMT	AHQLYQKKYQ	RYQHL IAA LQ	GFHAR IKEHT
IyHK-Hi	-VE ISQ ILN I	DRK IFLPDKN	QYSKYQHKKYH	RYLKF IEALK	NLD -----
IyHK-Ko	L				
IyHK-Ec	L				
IyHK-Hi	-				

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Figure 7

yiaQ-Ko	MSRPLLQLAL	DHTSLQAAQR	DVALLQDHVD	IVEAGTILCL	TEGLSAVKAL
yiaQ-Ec	MSRPLLQLAL	DHSSLEAAQR	DVTLLKDSVD	IVEAGTILCL	NEGLGAVKAL
yiaQ-Hi	MGKPLLQIAL	DAQYLETALV	DVKQIEHNID	ITIEVGILAC	SEGMRAVRIL

yiaQ-Ko	RAQCPGKIIV	ADWKVADAGE	TLAQQAFGAG	ANWMTIICAA	PLATVEKGHA
yiaQ-Ec	REQCPDKIIV	ADWKVADAGE	TLAQQAFGAG	ANWMTIICAA	PLATVEKGHA
yiaQ-Hi	RALYPNQILV	CDLKTTDAGA	TLAKMAFEAG	ADWLTVSAAA	HPATKAACQK

yiaQ-Ko	VAQA-----	---CGGEIQM	ELFGNWTLDD	ARAWYRTGVH	QA IYHRGRDA
yiaQ-Ec	MAQR-----	---CGGEIQI	ELFGNWTLDD	ARDWHRIGVR	QA IYHRGRDA
yiaQ-Hi	VAEEFNKIQP	NLGVPKEIQI	ELYGNWNFDE	VKNWLQLG IK	QA IYHRSRDA

yiaQ-Ko	QASGQQWGEA	DLARMKALSD	IGLELSITGG	ITPADLP LFK	DIN -VKAFIA
yiaQ-Ec	QASGQQWGEA	DLARMKALSD	IGLELSITGG	ITPADLP LFK	DIR -VKAFIA
yiaQ-Hi	ELSGLSWSNQ	DIENIEKLDS	LGIELSITGG	ITPDDLHLFK	NTKNLKAFIA

yiaQ-Ko	GRALAGAAHP	ARVAAEFHAQ	IDA IWGEQHA
yiaQ-Ec	GRALAGAANP	AQVAGDFHAQ	IDA IWGGARA
yiaQ-Hi	GRALVGKSGR	-EIAEQLKQK	IGQFW----I

00540"0624360

[illegible]

yiaR-Ko	FKTLRELNYR	GSFLIEMWTE	KASEPVLE II	QARRWIESRM	QEGGFTC
yiaR-Ec	FKTLHLNYR	GSFLIEMWTE	KAKEPVLE II	QARRWIEARM	QEAGFIC
yiaR-Hi	FSLLKKLNYR	GAFLIEMWTE	KNEEPLLE II	QARKWIVQOM	EKAGLLC

Parameter	Value	Unit
Temperature	25.0	°C
Pressure	1.0	atm
Flow rate	1.0	L/min
Concentration	0.1	mol/L
pH	7.0	
Wavelength	254	nm
Path length	1.0	cm
Sample volume	10	μL
Injection volume	1	μL
Retention time	10.5	min
Peak area	12345	arbitrary units
Peak height	1.2	absorbance
Baseline	0.1	absorbance
Resolution	1.5	min
Recovery	95	%
Stability	0.5	%
Linearity	0.999	R ²
Detection limit	0.01	μg/L
Quantification limit	0.05	μg/L
Accuracy	100	%
Precision	2.0	%
Correlation coefficient	0.999	R ²
Regression equation	y = 0.999x	
Intercept	0.001	
Slope	0.999	
Standard deviation	0.001	
Mean	0.001	
Variance	0.000	
Skewness	0.000	
Kurtosis	0.000	
Chi-square	0.000	
Degrees of freedom	1	
P-value	0.000	
F-value	0.000	
T-value	0.000	
W-value	0.000	
Z-value	0.000	
Y-value	0.000	
X-value	0.000	
Sum of squares	0.000	
Mean square	0.000	
Adjusted R-squared	0.999	
Adjusted F-value	0.000	
Adjusted T-value	0.000	
Adjusted W-value	0.000	
Adjusted Z-value	0.000	
Adjusted Y-value	0.000	
Adjusted X-value	0.000	
Adjusted Sum of squares	0.000	
Adjusted Mean square	0.000	
Adjusted Variance	0.000	
Adjusted Skewness	0.000	
Adjusted Kurtosis	0.000	
Adjusted Chi-square	0.000	
Adjusted Degrees of freedom	1	
Adjusted P-value	0.000	
Adjusted F-value	0.000	
Adjusted T-value	0.000	
Adjusted W-value	0.000	
Adjusted Z-value	0.000	
Adjusted Y-value	0.000	
Adjusted X-value	0.000	
Adjusted Sum of squares	0.000	
Adjusted Mean square	0.000	
Adjusted Variance	0.000	
Adjusted Skewness	0.000	
Adjusted Kurtosis	0.000	
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Adjusted Variance	0.000	
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Adjusted Kurtosis	0.000	
Adjusted Chi-square	0.000	
Adjusted Degrees of freedom	1	
Adjusted P-value	0.000	
Adjusted F-value	0.000	
Adjusted T-value	0.000	

yaS-Ko	RQW-PQLPDM	QSELLDKHYL	RKHGANAITG	KTSPAELPG
yaS-Ec	RQLAPQLPAM	QNELLDKHYL	RKHGANAYYG	Q-----
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Figure 10

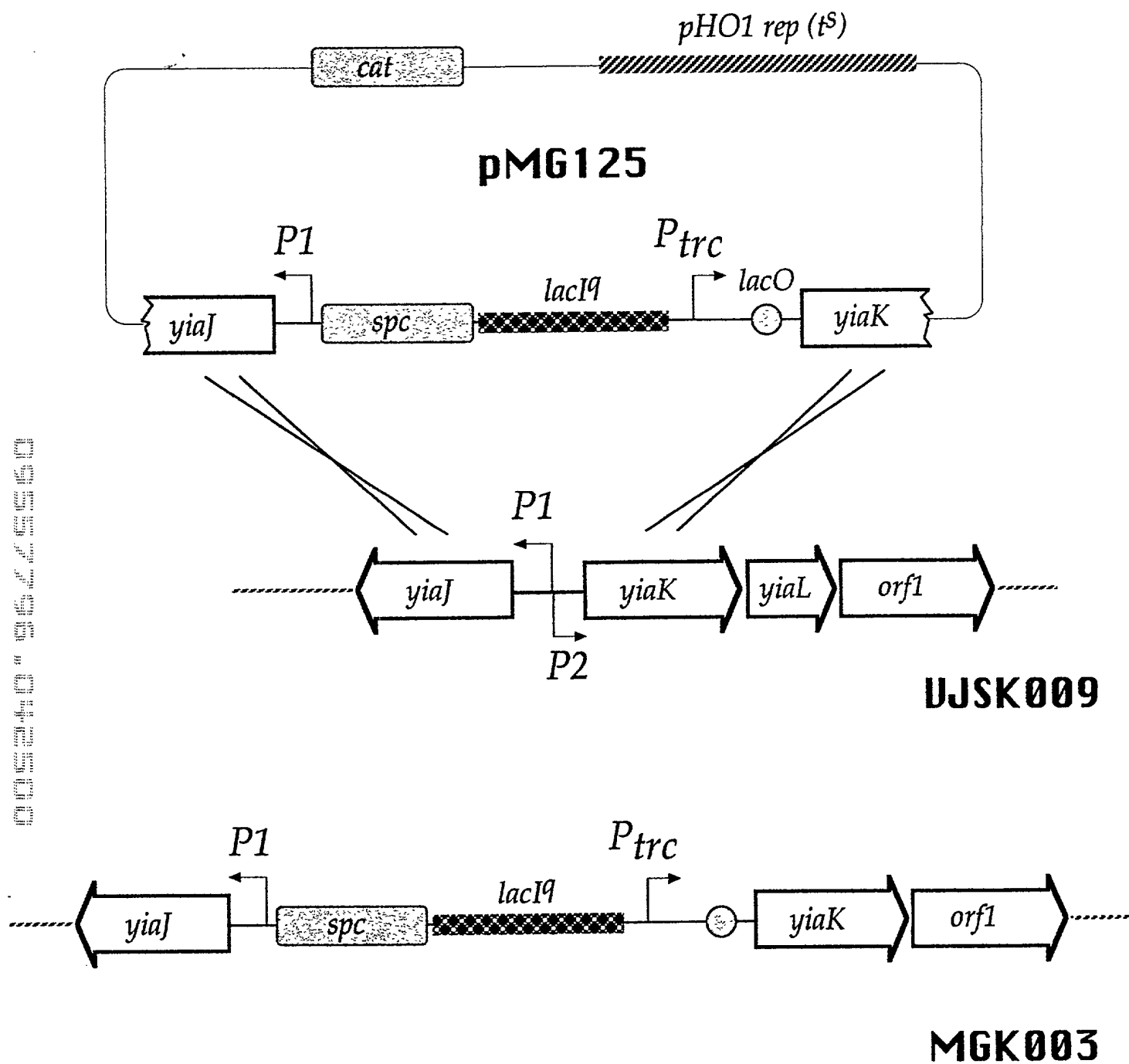
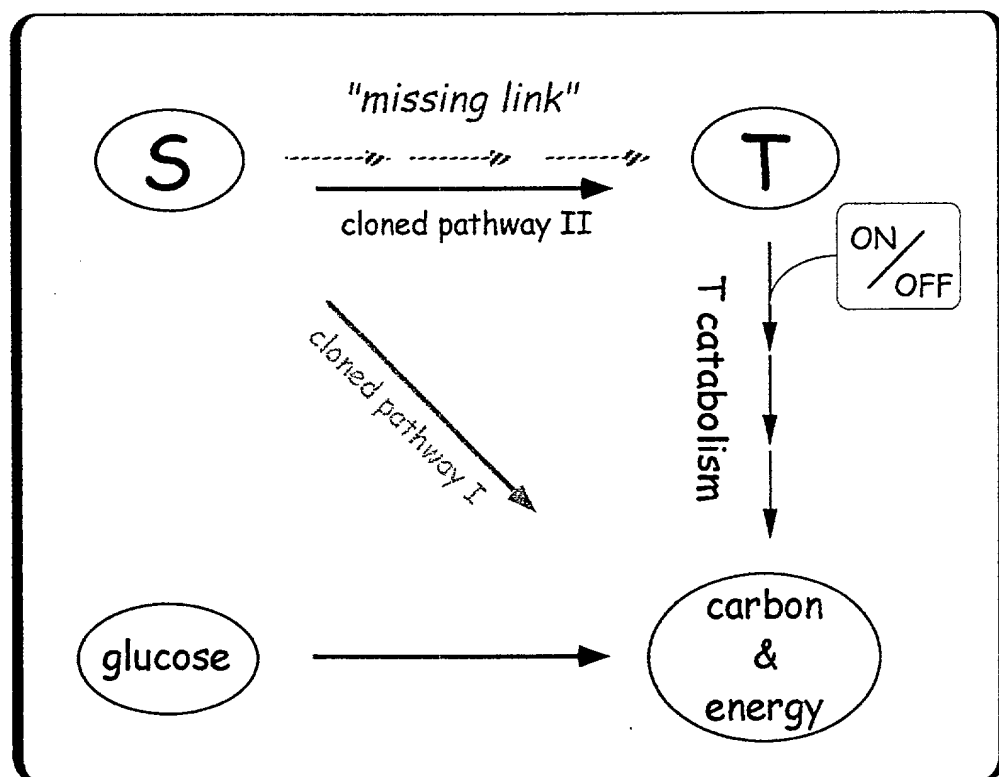
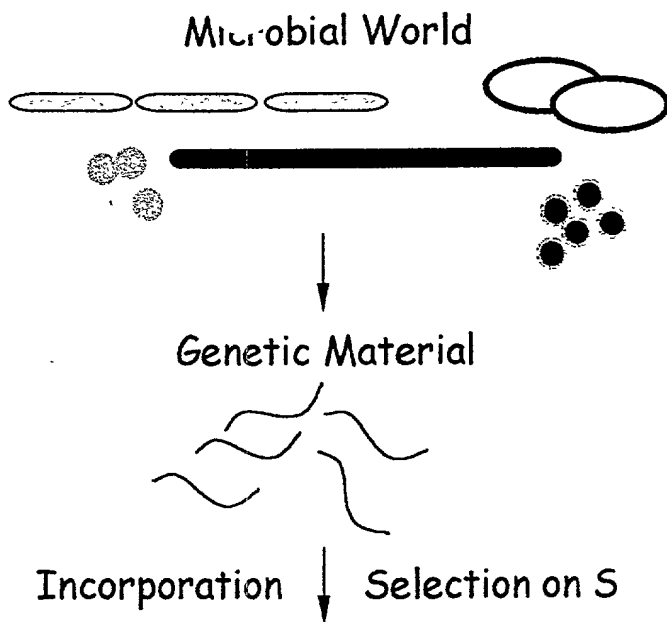
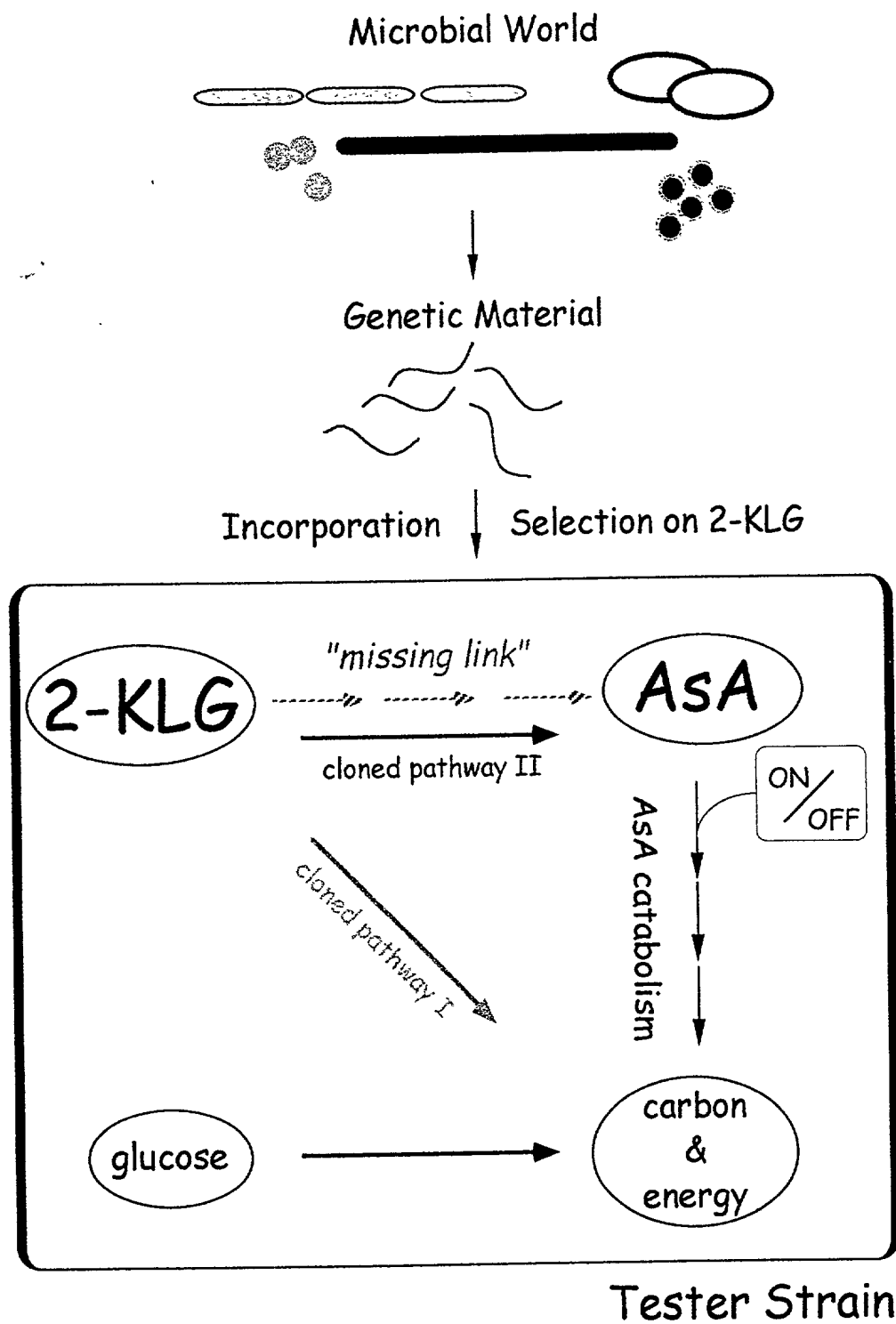


Figure 11



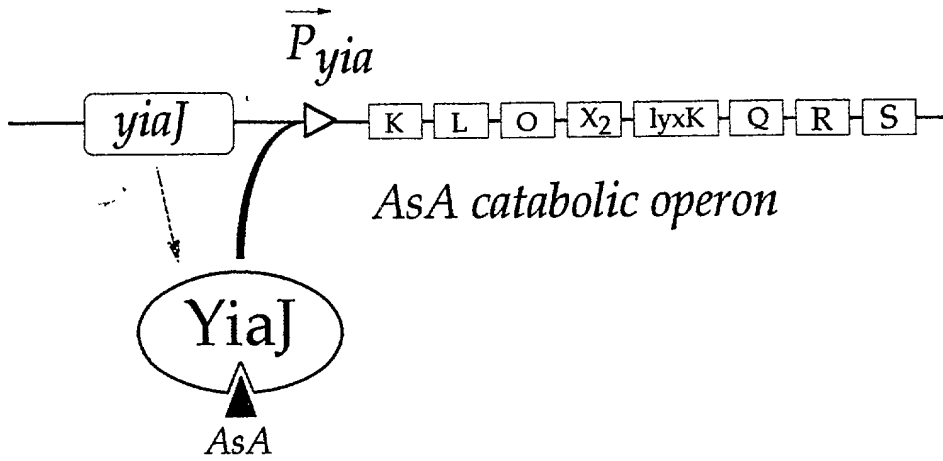
Tester Strain



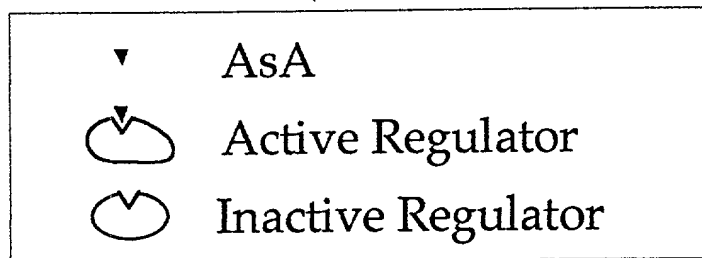
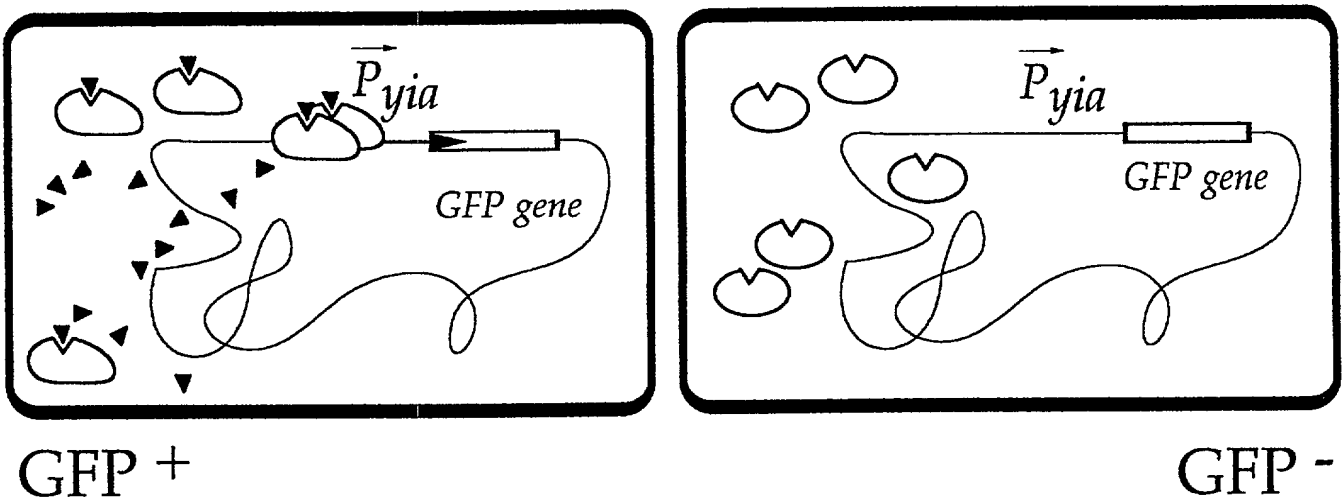
The Metabolic Selection Strategy

Figure 13

A



B



SEQUENCE LISTING

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Dartois, Veronique

<120> METABOLIC SELECTION METHODS

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<141> Herewith

<160> 33

<170> FastSEQ for Windows Version 3.0

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<213> yia j

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aaagatatca	acgtcaaagc	ctttattgcc	gggcgcgcgc	tggcaggcgc	cgcccatccg	600
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<210> 8
<211> 858
<212> DNA
<213> yia r

<400> 8

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accgatgaac	gcctttcgcg	cctggagtgg	accccggcc	agcgcgcac	gctggtgagc	180
gcgatgctgg	aaaccgcggt	cgccattccc	tcgatgtgct	tgtccgccca	tcgccgtttc	240
ccctttggca	gccgcgatga	agcggtagcg	gatcgggcgc	gagagattat	gaccaaagcc	300
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taogaagagc	atgatgaagg	caccggcgag	cgttttgccg	aagggtggc	ctgggcggta	420
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aactccatca	gcaaattgaa	aaagtgggac	gagatgcttt	cgtcaccgtg	gtttaccgtc	540
taccggagcg	tcggcaacct	cagcgcctgg	ggaaacgacg	tcaccgccga	gctgaagctg	600
ggcatcgatc	gtatcgccgc	catccacctg	aaagatacgc	tgcccgtgac	cgacgatagc	660
cctggccagt	tcgcgcacgt	gccgttcggc	gaaggatgcg	tcgattttgt	cggcattttt	720
aagacgctgc	gcgagctgaa	ctaccgcggt	tcatttttga	ttgagatgtg	gacggagaaa	780
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gaagggggat	tcacatgt					858

<210> 9
<211> 714
<212> DNA
<213> yia s

<400> 9

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<210> 10

<211> 272

<212> PRT

<213> YiaJ-Ko

<400> 10

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Met Gly Thr Lys Glu Ser Glu Asn Thr Gln Asp Lys Glu Arg Pro Ala
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Gly Ser Gln Ser Leu Phe Arg Gly Leu Met Leu Ile Glu Ile Leu Ser
      20              25              30

Asn Tyr Pro Asn Gly Cys Pro Val Ala His Leu Ser Glu Leu Ala Gly
      35              40              45

Leu Asn Lys Ser Thr Val His Arg Leu Leu Gln Gly Leu Gln Ser Cys
      50              55              60

Gly Tyr Val Thr Pro Ala Pro Ala Ala Gly Ser Tyr Ala Leu Thr Thr
      65              70              75              80

Lys Phe Ile Arg Val Gly Gln Lys Ala Leu Ser Ser Leu Asn Ile Ile
      85              90              95

His Val Ala Ala Pro His Leu Glu Ala Leu Asn Leu Ala Thr Gly Glu
      100             105             110

Thr Val Asn Phe Ser Ser Arg Glu Asp Asp His Ala Ile Leu Ile Tyr
      115             120             125

Lys Leu Glu Pro Thr Thr Gly Met Leu Arg Thr Arg Ala Tyr Ile Gly
      130             135             140

Gln His Met Arg Cys Thr Ala Arg Gln Trp Ala Lys Ile Tyr Met Ala
      145             150             155             160

Phe Gly His Pro Asp Tyr Val Glu Ser Tyr Trp Asn Ser His Gln Glu
      165             170             175

Ile Ile Gln Pro Leu Thr Arg Asn Thr Ile Thr Gly Leu Pro Ala Met
      180             185             190

His Asp Glu Leu Ala Gln Ile Arg Glu Arg Asn Met Ala Met Asp Arg
      195             200             205

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Glu Glu Asn Glu Leu Gly Val Ser Cys Leu Ala Val Pro Val Phe Asp
 210 215 220
 Ile His Gly Arg Val Pro Tyr Ala Ile Ser Ile Ser Leu Ser Thr Ser
 225 230 235 240
 Arg Leu Lys Gln Val Gly Glu Lys Asn Leu Leu Lys Pro Leu Arg Asp
 245 250 255
 Thr Ala Glu Ala Ile Ser Arg Glu Leu Gly Phe Ser Val Arg Glu Gly
 260 265 270

<210> 11
 <211> 332
 <212> PRT
 <213> YiaK-Ko

<400> 11

Met Lys Val Thr Phe Glu Gln Leu Lys Glu Ala Phe Asn Arg Val Leu
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 Leu Asp Ala Cys Val Ala Arg Glu Thr Ala Asp Ala Cys Ala Glu Met
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 Phe Ala Arg Thr Thr Glu Ser Gly Val Tyr Ser His Gly Val Asn Arg
 35 40 45
 Phe Pro Arg Phe Ile Gln Gln Leu Asp Asn Gly Asp Ile Ile Pro Glu
 50 55 60
 Ala Gln Pro Gln Arg Val Thr Thr Leu Gly Ala Ile Glu Gln Trp Asp
 65 70 75 80
 Ala Gln Arg Ser Ile Gly Asn Leu Thr Ala Lys Lys Met Met Asp Arg
 85 90 95
 Ala Ile Glu Leu Ala Ser Asp His Gly Ile Gly Leu Val Ala Leu Arg
 100 105 110
 Asn Ala Asn His Trp Met Arg Gly Gly Ser Tyr Gly Trp Gln Ala Ala
 115 120 125
 Glu Lys Gly Tyr Ile Gly Ile Cys Trp Thr Asn Ser Ile Ala Val Met
 130 135 140
 Ala Pro Trp Gly Ala Lys Glu Cys Arg Ile Gly Thr Asn Pro Leu Ile
 145 150 155 160
 Val Ala Ile Pro Ser Thr Pro Ile Thr Met Val Asp Met Ser Met Ser
 165 170 175
 Met Phe Ser Tyr Gly Met Leu Glu Val Asn Arg Leu Ala Gly Arg Glu
 180 185 190

Leu Pro Val Asp Gly Gly Phe Asp Asp Asp Gly Arg Leu Thr Lys Glu
 195 200 205
 Pro Gly Thr Ile Glu Lys Asn Arg Arg Ile Leu Pro Met Gly Tyr Trp
 210 215 220
 Lys Gly Ser Gly Leu Ser Ile Val Leu Asp Met Ile Ala Thr Leu Leu
 225 230 235 240
 Ser Asn Gly Ser Ser Val Ala Glu Val Thr Gln Glu Asn Ser Asp Glu
 245 250 255
 Tyr Gly Val Ser Gln Ile Phe Ile Ala Ile Glu Val Asp Lys Leu Ile
 260 265 270
 Asp Gly Ala Thr Arg Asp Ala Lys Leu Gln Arg Ile Met Asp Phe Ile
 275 280 285
 Thr Thr Ala Glu Arg Ala Asp Glu Asn Val Ala Val Arg Leu Pro Gly
 290 295 300
 His Glu Phe Thr Arg Leu Leu Asp Glu Asn Arg Arg Asn Gly Ile Thr
 305 310 315 320
 Val Asp Asp Ser Val Trp Ala Lys Ile Gln Ala Leu
 325 330

<210> 12

<211> 154

<212> PRT

<213> YiaL-Ko

<400> 12

Met Ile Phe Gly His Ile Ala Gln Pro Asn Pro Cys Arg Leu Pro Ala
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 Ala Ile Glu Arg Ala Leu Asp Phe Leu Arg Thr Thr Asp Phe His Ala
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 Leu Ala Pro Gly Val Val Glu Ile Asp Gly Gln Asn Ile Phe Ala Gln
 35 40 45
 Val Ile Asp Leu Thr Thr Arg Asp Ala Ala Glu Asn Arg Pro Glu Val
 50 55 60
 His Arg Arg Tyr Leu Asp Ile Gln Phe Leu Ala Ser Gly Glu Glu Lys
 65 70 75 80
 Ile Gly Ile Ala Ile Asp Thr Gly Asn Asn Gln Ile Ser Glu Ser Leu
 85 90 95
 Leu Glu Gln Arg Asp Ile Ile Phe Tyr His Asp Ser Glu His Glu Ser
 100 105 110

Phe Phe Glu Met Thr Pro Gly Asn Tyr Ala Ile Phe Phe Pro Gln Asp
 115 120 125

Val His Arg Pro Gly Cys Asn Lys Thr Val Ala Thr Pro Ile Arg Lys
 130 135 140

Ile Val Val Lys Val Ala Ile Ser Val Leu
 145 150

<210> 13
 <211> 315
 <212> PRT
 <213> ORF1

<400> 13

Met Asn Ser Asn Asn Thr Gly Tyr Ile Ile Gly Ala Tyr Pro Cys Ala
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Pro Cys Ala Pro Ser Phe His Gln Lys Ser Glu Glu Glu Glu Met Glu
 20 25 30

Phe Trp Arg Gln Leu Ser Asp Thr Pro Asp Ile Arg Gly Leu Glu Gln
 35 40 45

Pro Cys Leu Pro Cys Leu Glu His Leu His Pro Leu Gly Asp Glu Trp
 50 55 60

Leu Leu Arg His Thr Pro Gly His Trp Gln Ile Val Val Thr Ala Ile
 65 70 75 80

Met Glu Thr Met Arg Arg Arg Gly Glu Asn Gly Gly Phe Gly Leu Ala
 85 90 95

Ser Ser Asp Glu Thr Gln Arg Lys Ala Cys Val Glu Tyr Tyr Arg His
 100 105 110

Leu Gln Gln Lys Ile Ala Lys Ile Asn Gly Asn Thr Ala Gly Lys Val
 115 120 125

Ile Ala Leu Glu Leu His Ala Ala Pro Leu Ala Gly Asn Ala Asn Val
 130 135 140

Ala Gln Ala Thr Asp Ala Phe Ala Arg Ser Leu Lys Glu Ile Thr Arg
 145 150 155 160

Trp Asp Trp Ser Cys Glu Leu Val Leu Glu His Cys Asp Ala Met Thr
 165 170 175

Gly Ser Ala Pro Arg Lys Gly Phe Leu Pro Leu Glu Asn Val Leu Glu
 180 185 190

Ala Ile Ala Asp Tyr Asp Val Gly Ile Cys Ile Asn Trp Ala Arg Ser
 195 200 205

Ala Ile Glu Gly Arg Asn Thr Val Leu Pro Leu Thr His Thr Gln Gln
 210 215 220

Val Lys Arg Ala Gly Lys Leu Gly Ala Leu Met Phe Ser Gly Thr Thr
 225 230 235 240

Gln Thr Gly Glu Tyr Gly Glu Trp Gln Asp Leu His Ala Pro Phe Ala
 245 250 255

Pro Phe Cys Pro Gln Ser Leu Met Thr Thr Glu His Ala Arg Glu Leu
 260 265 270

Phe Ala Cys Ala Gly Thr Ala Pro Leu Gln Phe Ser Gly Ile Lys Leu
 275 280 285

Leu Glu Ile Asn Ala Ser Ala Asn Val Asp His Arg Ile Ala Ile Leu
 290 295 300

Arg Asp Gly Ile Ser Ala Leu Lys Gln Ala Gln
 305 310 315

<210> 14
 <211> 439
 <212> PRT
 <213> YiaX2

<400> 14

Met Asn Ile Thr Ser Asn Ser Thr Thr Lys Asp Ile Pro Arg Gln Arg
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Trp Leu Arg Ile Ile Pro Pro Ile Leu Ile Thr Cys Ile Ile Ser Tyr
 20 25 30

Met Asp Arg Val Asn Ile Ala Phe Ala Met Pro Gly Gly Met Asp Ala
 35 40 45

Asp Leu Gly Ile Ser Ala Thr Met Ala Gly Leu Ala Gly Gly Ile Phe
 50 55 60

Phe Ile Gly Tyr Leu Phe Leu Gln Val Pro Gly Gly Lys Ile Ala Val
 65 70 75 80

His Gly Ser Gly Lys Lys Phe Ile Gly Trp Ser Leu Val Ala Trp Ala
 85 90 95

Val Ile Ser Val Leu Thr Gly Leu Ile Thr Asn Gln Tyr Gln Leu Leu
 100 105 110

Ala Leu Arg Phe Leu Leu Gly Val Ala Glu Gly Gly Met Leu Pro Val
 115 120 125

Val Leu Thr Met Ile Ser Asn Trp Phe Pro Asp Ala Glu Arg Gly Arg
 130 135 140

Ala Asn Ala Ile Val Ile Met Phe Val Pro Ile Ala Gly Ile Ile Thr
 145 150 155 160
 Ala Pro Leu Ser Gly Trp Ile Ile Thr Val Leu Asp Trp Arg Trp Leu
 165 170 175
 Phe Ile Ile Glu Gly Leu Leu Ser Leu Val Val Leu Val Leu Trp Ala
 180 185 190
 Tyr Thr Ile Tyr Asp Arg Pro Gln Glu Ala Arg Trp Ile Ser Glu Ala
 195 200 205
 Glu Lys Arg Tyr Leu Val Glu Thr Leu Ala Ala Glu Gln Lys Ala Ile
 210 215 220
 Ala Gly Thr Glu Val Lys Asn Ala Ser Leu Ser Ala Val Leu Ser Asp
 225 230 235 240
 Lys Thr Met Trp Gln Leu Ile Ala Leu Asn Phe Phe Tyr Gln Thr Gly
 245 250 255
 Ile Tyr Gly Tyr Thr Leu Trp Leu Pro Thr Ile Leu Lys Glu Leu Thr
 260 265 270
 His Ser Ser Met Gly Gln Val Gly Met Leu Ala Ile Leu Pro Tyr Val
 275 280 285
 Gly Ala Ile Ala Gly Met Phe Leu Phe Ser Ser Leu Ser Asp Arg Thr
 290 295 300
 Gly Lys Arg Lys Leu Phe Val Cys Leu Pro Leu Ile Gly Phe Ala Leu
 305 310 315 320
 Cys Met Phe Leu Ser Val Ala Leu Lys Asn Gln Ile Trp Leu Ser Tyr
 325 330 335
 Ala Ala Leu Val Gly Cys Gly Phe Phe Leu Gln Ser Ala Ala Gly Val
 340 345 350
 Phe Trp Thr Ile Pro Ala Arg Leu Phe Ser Ala Glu Met Ala Gly Gly
 355 360 365
 Ala Arg Gly Val Ile Asn Ala Leu Gly Asn Leu Gly Gly Phe Cys Gly
 370 375 380
 Pro Tyr Ala Val Gly Val Leu Ile Thr Leu Tyr Ser Lys Asp Ala Gly
 385 390 395 400
 Val Tyr Cys Leu Ala Ile Ser Leu Ala Leu Ala Ala Leu Met Ala Leu
 405 410 415
 Leu Leu Pro Ala Lys Cys Asp Ala Gly Ala Ala Pro Val Lys Thr Ile
 420 425 430
 Asn Pro His Lys Arg Thr Ala
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<210> 15
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 <212> PRT
 <213> LyxK-Ko

<400> 15

Met	Ser	Lys	Lys	Gln	Ala	Phe	Trp	Leu	Gly	Ile	Asp	Cys	Gly	Gly	Thr	1		5		10				15
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Val	Arg	Gln	Ala	Leu	Arg	Thr	Met	Ser	Pro	Leu	Pro	Gly	Tyr	Ala	Glu		35		40				45	
Arg	Asp	Met	Arg	Gln	Leu	Trp	Gln	His	Cys	Ala	Ala	Thr	Ile	Ala	Gly	50			55			60		
Leu	Leu	Gln	Gln	Ala	Gly	Val	Ser	Gly	Glu	Gln	Ile	Lys	Gly	Val	Gly	65			70			75		80
Ile	Ser	Ala	Gln	Gly	Gln	Gly	Leu	Phe	Leu	Leu	Asp	Lys	Gln	Asp	Arg		85			90			95	
Pro	Leu	Gly	Asn	Ala	Ile	Leu	Ser	Ser	Asp	Arg	Arg	Ala	Leu	Lys	Ile		100		105				110	
Val	Gln	Arg	Trp	Gln	Arg	Asp	Arg	Ile	Pro	Glu	Arg	Leu	Tyr	Pro	Val		115		120				125	
Thr	Arg	Gln	Thr	Leu	Trp	Thr	Gly	His	Pro	Ala	Ser	Leu	Leu	Arg	Trp		130		135				140	
Val	Lys	Glu	Asn	Glu	Pro	Gln	Arg	Tyr	Ala	Gln	Ile	Gly	Cys	Val	Met	145			150			155		160
Met	Gly	His	Asp	Tyr	Leu	Arg	Trp	Cys	Leu	Thr	Gly	Ala	Lys	Gly	Cys		165			170			175	
Glu	Glu	Ser	Asn	Ile	Ser	Glu	Ser	Asn	Leu	Tyr	Asn	Met	Ala	Met	Gly		180			185			190	
Gln	Tyr	Asp	Pro	Arg	Leu	Thr	Glu	Trp	Leu	Gly	Ile	Gly	Glu	Ile	Asp		195		200			205		
Ser	Ala	Leu	Pro	Pro	Val	Val	Gly	Ser	Ala	Glu	Ile	Cys	Gly	Glu	Ile	210			215			220		
Thr	Ala	Gln	Ala	Ala	Ala	Leu	Thr	Gly	Leu	Ala	Ala	Gly	Thr	Pro	Val	225			230			235		240
Val	Gly	Gly	Leu	Phe	Asp	Val	Val	Ser	Thr	Ala	Leu	Cys	Ala	Gly	Ile		245			250			255	
Glu	Asp	Glu	Ser	Thr	Leu	Asn	Ala	Val	Met	Gly	Thr	Trp	Ala	Val	Thr		260			265			270	

Ser Gly Ile Ala His Gly Leu Arg Asp His Glu Ala His Pro Tyr Val
 275 280 285
 Tyr Gly Arg Tyr Val Asn Asp Gly Gln Tyr Ile Val His Glu Ala Ser
 290 295 300
 Pro Thr Ser Ser Gly Asn Leu Glu Trp Phe Thr Ala Gln Trp Gly Asp
 305 310 315 320
 Leu Ser Phe Asp Glu Ile Asn Gln Ala Val Ala Ser Leu Pro Lys Ala
 325 330 335
 Gly Ser Glu Leu Phe Phe Leu Pro Phe Leu Tyr Gly Ser Asn Ala Gly
 340 345 350
 Leu Glu Met Thr Cys Gly Phe Tyr Gly Met Gln Ala Leu His Thr Arg
 355 360 365
 Ala His Leu Leu Gln Ala Val Tyr Glu Gly Val Val Phe Ser His Met
 370 375 380
 Thr His Leu Ser Arg Met Arg Glu Arg Phe Thr Asn Val Gln Ala Leu
 385 390 395 400
 Arg Val Thr Gly Gly Pro Ala His Ser Asp Val Trp Met Gln Met Leu
 405 410 415
 Ala Asp Val Ser Gly Leu Arg Ile Glu Leu Pro Lys Val Glu Glu Thr
 420 425 430
 Gly Cys Phe Gly Ala Ala Leu Ala Ala Arg Val Gly Thr Gly Val Tyr
 435 440 445
 Arg Ser Phe Ser Glu Ala Arg Arg Ala Arg Gln His Pro Val Arg Thr
 450 455 460
 Leu Leu Pro Asp Met Thr Ala His Ala Arg Tyr Gln Arg Lys Tyr Arg
 465 470 475 480
 His Tyr Leu His Leu Ile Glu Ala Leu Gln Gly Tyr His Ala Arg Ile
 485 490 495
 Lys Glu His Ala Leu
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<210> 16
 <211> 220
 <212> PRT
 <213> YiaQ-Ko

<400> 16

Met Ser Arg Pro Leu Leu Gln Leu Ala Leu Asp His Thr Ser Leu Gln
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Ala Ala Gln Arg Asp Val Ala Leu Leu Gln Asp His Val Asp Ile Val
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 Glu Ala Gly Thr Ile Leu Cys Leu Thr Glu Gly Leu Ser Ala Val Lys
 35 40 45
 Ala Leu Arg Ala Gln Cys Pro Gly Lys Ile Ile Val Ala Asp Trp Lys
 50 55 60
 Val Ala Asp Ala Gly Glu Thr Leu Ala Gln Gln Ala Phe Gly Ala Gly
 65 70 75 80
 Ala Asn Trp Met Thr Ile Ile Cys Ala Ala Pro Leu Ala Thr Val Glu
 85 90 95
 Lys Gly His Ala Val Ala Gln Ala Cys Gly Gly Glu Ile Gln Met Glu
 100 105 110
 Leu Phe Gly Asn Trp Thr Leu Asp Asp Ala Arg Ala Trp Tyr Arg Thr
 115 120 125
 Gly Val His Gln Ala Ile Tyr His Arg Gly Arg Asp Ala Gln Ala Ser
 130 135 140
 Gly Gln Gln Trp Gly Glu Ala Asp Leu Ala Arg Met Lys Ala Leu Ser
 145 150 155 160
 Asp Ile Gly Leu Glu Leu Ser Ile Thr Gly Gly Ile Thr Pro Ala Asp
 165 170 175
 Leu Pro Leu Phe Lys Asp Ile Asn Val Lys Ala Phe Ile Ala Gly Arg
 180 185 190
 Ala Leu Ala Gly Ala Ala His Pro Ala Arg Val Ala Ala Glu Phe His
 195 200 205
 Ala Gln Ile Asp Ala Ile Trp Gly Glu Gln His Ala
 210 215 220

<210> 17
 <211> 286
 <212> PRT
 <213> YiaR-Ko

<400> 17

Met Arg Asn His Pro Leu Gly Ile Tyr Glu Lys Ala Leu Ala Lys Asp
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 Leu Ser Trp Pro Glu Arg Leu Val Leu Ala Lys Ser Cys Gly Phe Asp
 20 25 30
 Phe Val Glu Met Ser Val Asp Glu Thr Asp Glu Arg Leu Ser Arg Leu
 35 40 45

Glu Trp Thr Pro Ala Gln Arg Ala Ser Leu Val Ser Ala Met Leu Glu
 50 55 60
 Thr Ala Val Ala Ile Pro Ser Met Cys Leu Ser Ala His Arg Arg Phe
 65 70 75 80
 Pro Phe Gly Ser Arg Asp Glu Ala Val Arg Asp Arg Ala Arg Glu Ile
 85 90 95
 Met Thr Lys Ala Ile Arg Leu Ala Arg Asp Leu Gly Ile Arg Thr Ile
 100 105 110
 Gln Leu Ala Gly Tyr Asp Val Tyr Tyr Glu Glu His Asp Glu Gly Thr
 115 120 125
 Arg Gln Arg Phe Ala Glu Gly Leu Ala Trp Ala Val Glu Gln Ala Ala
 130 135 140
 Ala Ala Gln Val Met Leu Ala Val Glu Ile Met Asp Thr Ala Phe Met
 145 150 155 160
 Asn Ser Ile Ser Lys Trp Lys Lys Trp Asp Glu Met Leu Ser Ser Pro
 165 170 175
 Trp Phe Thr Val Tyr Pro Asp Val Gly Asn Leu Ser Ala Trp Gly Asn
 180 185 190
 Asp Val Thr Ala Glu Leu Lys Leu Gly Ile Asp Arg Ile Ala Ala Ile
 195 200 205
 His Leu Lys Asp Thr Leu Pro Val Thr Asp Asp Ser Pro Gly Gln Phe
 210 215 220
 Arg Asp Val Pro Phe Gly Glu Gly Cys Val Asp Phe Val Gly Ile Phe
 225 230 235 240
 Lys Thr Leu Arg Glu Leu Asn Tyr Arg Gly Ser Phe Leu Ile Glu Met
 245 250 255
 Trp Thr Glu Lys Ala Ser Glu Pro Val Leu Glu Ile Ile Gln Ala Arg
 260 265 270
 Arg Trp Ile Glu Ser Arg Met Gln Glu Gly Gly Phe Thr Cys
 275 280 285

<210> 18
 <211> 238
 <212> PRT
 <213> YiaS-Ko

<400> 18

Met Leu Glu Gln Leu Lys Ala Glu Val Leu Ala Ala Asn Leu Ala Leu
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Pro Ala His Gly Leu Val Thr Phe Thr Trp Gly Asn Val Ser Ala Val
 20 25 30
 Asp Glu Thr Arg Lys Leu Met Val Ile Lys Pro Ser Gly Val Glu Tyr
 35 40 45
 Glu Val Met Thr Ala Asp Asp Met Val Val Val Glu Met Ala Ser Gly
 50 55 60
 Lys Val Val Glu Gly Gly Lys Lys Pro Ser Ser Asp Thr Pro Thr His
 65 70 75 80
 Leu Ala Leu Tyr Arg Arg Tyr Pro Gln Ile Gly Gly Ile Val His Thr
 85 90 95
 His Ser Arg His Ala Thr Ile Trp Ser Gln Ala Gly Leu Asp Leu Pro
 100 105 110
 Ala Trp Gly Thr Thr His Ala Asp Tyr Phe Tyr Gly Ala Ile Pro Cys
 115 120 125
 Thr Arg Arg Met Thr Val Glu Glu Ile Asn Gly Glu Tyr Glu Tyr Gln
 130 135 140
 Thr Gly Glu Val Ile Ile Lys Thr Phe Glu Gln Arg Gly Leu Asp Pro
 145 150 155 160
 Ala Gln Ile Pro Ala Val Leu Val His Ser His Gly Pro Phe Ala Trp
 165 170 175
 Gly Lys Asp Ala Ala Asp Ala Val His Asn Ala Val Val Leu Glu Glu
 180 185 190
 Cys Ala Tyr Met Gly Leu Phe Ser Arg Gln Trp Pro Gln Leu Pro Asp
 195 200 205
 Met Gln Ser Glu Leu Leu Asp Lys His Tyr Leu Arg Lys His Gly Ala
 210 215 220
 Asn Ala Ile Thr Gly Lys Thr Ser Pro Ala Glu Leu Pro Gly
 225 230 235

<210> 19
 <211> 9334
 <212> DNA
 <213> yia

<400> 19

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35 40 45

Ser Glu Leu Ala Gly Leu Asn Lys Ser Thr Val His Arg Leu Leu Gln
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 Gly Leu Gln Ser Cys Gly Tyr Val Thr Thr Ala Pro Ala Ala Gly Ser
 65 70 75 80
 Tyr Arg Leu Thr Thr Lys Phe Ile Ala Val Gly Gln Lys Ala Leu Ser
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 Ser Leu Asn Ile Ile His Ile Ala Ala Pro His Leu Glu Ala Leu Asn
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 Ile Ala Thr Gly Glu Thr Ile Asn Phe Ser Ser Arg Glu Asp Asp His
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 Ala Ile Leu Ile Tyr Lys Leu Glu Pro Thr Thr Gly Met Leu Arg Thr
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 Arg Ala Tyr Ile Gly Gln His Met Pro Leu Tyr Cys Ser Ala Met Gly
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 Lys Ile Tyr Met Ala Phe Gly His Pro Asp Tyr Val Lys Ser Tyr Trp
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 Glu Ser His Gln His Glu Ile Gln Pro Leu Thr Arg Asn Thr Ile Thr
 180 185 190
 Glu Leu Pro Ala Met Phe Asp Glu Leu Ala His Ile Arg Glu Ser Gly
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 Ala Ala Met Asp Arg Glu Glu Asn Glu Leu Gly Val Ser Cys Ile Ala
 210 215 220
 Val Pro Val Phe Asp Ile His Gly Arg Val Pro Tyr Ala Val Ser Ile
 225 230 235 240
 Ser Leu Ser Thr Ser Arg Leu Lys Gln Val Gly Glu Lys Asn Leu Leu
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 Asn Gly Cys Pro Leu Ala Lys Leu Ala Glu Leu Ala Asn Leu Asn Lys
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 Ser Thr Ala His Arg Leu Leu Gln Gly Leu Gln Asn Glu Gly Tyr Val
 50 55 60
 Lys Pro Ala Asn Ala Ala Gly Ser Tyr Arg Leu Thr Ile Lys Cys Leu
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 Ser Ile Gly Gln Lys Val Leu Ser Ser Met Asn Ile Ile His Val Ala
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 Ser Pro Tyr Leu Glu Gln Leu Asn Leu Lys Leu Gly Glu Thr Ile Asn
 100 105 110
 Phe Ser Lys Arg Glu Asp Asp His Ala Ile Met Ile Tyr Lys Leu Glu
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 Pro Thr Asn Gly Met Leu Lys Thr Arg Ala Tyr Ile Gly Gln Tyr Leu
 130 135 140
 Lys Leu Tyr Cys Ser Ala Met Gly Lys Ile Phe Leu Ala Tyr Glu Lys
 150 155 160
 Lys Val Asp Tyr Leu Ser His Tyr Trp Gln Ser His Gln Arg Glu Ile
 165 170 175
 Lys Lys Leu Thr Arg Tyr Thr Ile Thr Glu Leu Asp Asp Ile Lys Leu
 180 185 190
 Glu Leu Glu Thr Ile Arg Gln Thr Ala Tyr Ala Met Asp Arg Glu Glu
 195 200 205
 Asn Glu Leu Gly Val Thr Cys Ile Ala Cys Pro Ile Phe Asp Ser Phe
 210 215 220
 Gly Gln Val Glu Tyr Ala Ile Ser Val Ser Met Ser Ile Tyr Arg Leu
 225 230 235 240
 Asn Lys Phe Gly Thr Asp Ala Phe Leu Gln Glu Ile Arg Lys Thr Ala
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 Glu Gln Ile Ser Leu Glu Leu Gly Tyr Glu Asn Ile
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 35 40 45
 Phe Pro Arg Phe Ile Gln Gln Leu Glu Asn Gly Asp Ile Ile Pro Asp
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 Ala Gln Pro Lys Arg Ile Thr Ser Leu Gly Ala Ile Glu Gln Trp Asp
 65 70 75 80
 Ala Gln Arg Ser Ile Gly Asn Leu Thr Ala Lys Lys Met Met Asp Arg
 85 90 95
 Ala Ile Glu Leu Ala Ala Asp His Gly Ile Gly Leu Val Ala Leu Arg
 100 105 110
 Asn Ala Asn His Trp Met Arg Gly Gly Ser Tyr Gly Trp Gln Ala Ala
 115 120 125
 Glu Lys Gly Tyr Ile Gly Ile Cys Trp Thr Asn Ser Ile Ala Val Met
 130 135 140
 Pro Pro Trp Gly Ala Lys Glu Cys Arg Ile Gly Thr Asn Pro Leu Ile
 145 150 155 160
 Val Ala Ile Pro Ser Thr Pro Ile Thr Met Val Asp Met Ser Met Ser
 165 170 175
 Met Phe Ser Tyr Gly Met Leu Glu Val Asn Arg Leu Ala Gly Arg Gln
 180 185 190
 Leu Pro Val Asp Gly Gly Phe Asp Asp Glu Gly Asn Leu Thr Lys Glu
 195 200 205
 Pro Gly Val Ile Glu Lys Asn Arg Arg Ile Leu Pro Met Gly Tyr Trp
 210 215 220
 Lys Gly Ser Gly Met Ser Ile Val Leu Asp Met Ile Ala Thr Leu Leu
 225 230 235 240
 Ser Asp Gly Ala Ser Val Ala Glu Val Thr Gln Asp Asn Ser Asp Glu
 245 250 255
 Tyr Gly Ile Ser Gln Ile Phe Ile Ala Ile Glu Val Asp Lys Leu Ile
 260 265 270
 Asp Gly Pro Thr Arg Asp Ala Lys Leu Gln Arg Ile Met Asp Tyr Val
 275 280 285

Thr Ser Ala Glu Arg Ala Asp Glu Asn Gln Ala Ile Arg Leu Pro Gly
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His Glu Phe Thr Thr Leu Leu Ala Glu Asn Arg Arg Asn Gly Ile Thr
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Val Asp Asp Ser Val Trp Ala Lys Ile Gln Ala Leu
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<210> 23

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<400> 23

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 20 25 30

Phe Thr Asp Thr Thr Gln Ala Gly Ala Tyr Ser His Gly Ile Asn Arg
 35 40 45

Phe Pro Arg Phe Ile Gln Gln Leu Glu Gln Gly Asp Ile Val Pro Asn
 50 55 60

Ala Ile Pro Thr Lys Val Leu Ser Leu Gly Ser Ile Glu Gln Trp Asp
 65 70 75 80

Ala His Gln Ala Ile Gly Asn Leu Thr Ala Lys Lys Met Met Asp Arg
 85 90 95

Ala Ile Glu Leu Ala Ser Gln His Gly Val Gly Val Ile Ala Leu Arg
 100 105 110

Asn Ala Asn His Trp Met Arg Gly Gly Ser Tyr Gly Trp Gln Ala Ala
 115 120 125

Glu Lys Gly Tyr Ile Gly Ile Cys Trp Thr Asn Ala Leu Ala Val Met
 130 135 140

Pro Pro Trp Gly Ala Lys Glu Cys Arg Ile Gly Thr Asn Pro Leu Ile
 145 150 155 160

Ile Ala Val Pro Thr Thr Pro Ile Thr Met Val Asp Met Ser Cys Ser
 165 170 175

Met Tyr Ser Tyr Gly Met Leu Glu Val His Arg Leu Ala Gly Arg Gln
 180 185 190

Thr Phe Val Asp Ala Gly Phe Asp Asp Glu Gly Asn Leu Thr Arg Asp
 195 200 205

Pro Ser Ile Val Glu Lys Asn Arg Arg Leu Leu Pro Met Gly Phe Trp
 210 215 220
 Lys Gly Ser Gly Leu Ser Ile Val Leu Asp Met Ile Ala Thr Leu Leu
 225 230 235 240
 Ser Asn Gly Glu Ser Thr Val Ala Val Thr Glu Asp Lys Asn Asp Glu
 245 250 255
 Tyr Cys Val Ser Gln Val Phe Ile Ala Ile Glu Val Asp Arg Leu Ile
 260 265 270
 Asp Gly Lys Ser Lys Asp Glu Lys Leu Asn Arg Ile Met Asp Tyr Val
 275 280 285
 Lys Thr Ala Glu Arg Ser Asp Pro Thr Gln Ala Val Arg Leu Pro Gly
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 His Glu Phe Thr Thr Ile Leu Ser Asp Asn Gln Thr Asn Gly Ile Pro
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 Val Asp Glu Arg Val Trp Ala Lys Leu Lys Thr Leu
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 35 40 45
 Ile Ile Asp Leu Thr Thr Arg Glu Ala Val Val Asn Arg Pro Glu Val
 50 55 60
 His Arg Arg Tyr Ile Asp Ile Gln Phe Leu Ala Trp Gly Glu Glu Lys
 65 70 75 80
 Ile Gly Ile Ala Ile Asp Thr Gly Asn Asn Lys Val Ser Glu Ser Leu
 85 90 95
 Leu Glu Gln Arg Asn Ile Ile Phe Tyr His Asp Ser Glu His Glu Ser
 100 105 110
 Phe Ile Glu Met Ile Pro Gly Ser Tyr Ala Ile Phe Phe Pro Gln Asp
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Val His Arg Pro Gly Cys Ile Met Gln Thr Ala Ser Glu Ile Arg Lys
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Ile Val Val Lys Val Ala Leu Thr Ala Leu Asn
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<210> 25
<211> 155
<212> PRT
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<400> 25

Met Ile Ile Ser Ser Leu Thr Asn Pro Asn Phe Lys Val Gly Leu Pro
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Lys Val Ile Ala Glu Val Cys Asp Tyr Leu Asn Thr Leu Asp Leu Asn
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Ala Leu Glu Asn Gly Arg His Asp Ile Asn Asp Gln Ile Tyr Met Asn
35 40 45

Val Met Glu Pro Glu Thr Ala Glu Pro Ser Ser Lys Lys Ala Glu Leu
50 55 60

His His Glu Tyr Leu Asp Val Gln Val Leu Ile Arg Gly Thr Glu Asn
65 70 75 80

Ile Glu Val Gly Ala Thr Tyr Pro Asn Leu Ser Lys Tyr Glu Asp Tyr
85 90 95

Asn Glu Ala Asp Asp Tyr Gln Leu Cys Ala Asp Ile Asp Asp Lys Phe
100 105 110

Thr Val Thr Met Lys Pro Lys Met Phe Ala Val Phe Tyr Pro Tyr Glu
115 120 125

Pro His Lys Pro Cys Cys Val Val Asn Gly Lys Thr Glu Lys Ile Lys
130 135 140

Lys Leu Val Val Lys Val Pro Val Lys Leu Ile
145 150 155

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 Pro Leu Cys Ala Leu Ser Pro Gln Pro Gly Trp Ala Glu Arg Asp Met
 35 40 45
 Ala Glu Leu Trp Gln Cys Cys Met Ala Val Ile Arg Ala Leu Leu Thr
 50 55 60
 His Ser Gly Val Ser Gly Glu Gln Ile Val Gly Ile Gly Ile Ser Ala
 65 70 75 80
 Gln Gly Lys Gly Leu Phe Leu Leu Asp Lys Asn Asp Lys Pro Leu Gly
 85 90 95
 Asn Ala Ile Leu Ser Ser Asp Arg Arg Ala Met Glu Ile Val Arg Arg
 100 105 110
 Trp Gln Glu Asp Gly Ile Pro Glu Lys Leu Tyr Pro Leu Thr Arg Gln
 115 120 125
 Thr Leu Trp Thr Gly His Pro Val Ser Leu Leu Arg Trp Leu Lys Glu
 130 135 140
 His Glu Pro Glu Arg Tyr Ala Gln Ile Gly Cys Val Met Met Thr His
 145 150 155 160
 Asp Tyr Leu Arg Trp Cys Leu Thr Gly Val Lys Gly Cys Glu Glu Ser
 165 170 175
 Asn Ile Ser Glu Ser Asn Leu Tyr Asn Met Ser Leu Gly Glu Tyr Asp
 180 185 190
 Pro Cys Leu Thr Asp Trp Leu Gly Ile Ala Glu Ile Asn His Ala Leu
 195 200 205
 Pro Pro Val Val Gly Ser Ala Glu Ile Cys Gly Glu Ile Thr Ala Gln
 210 215 220
 Thr Ala Ala Leu Thr Gly Leu Lys Ala Gly Thr Pro Val Val Gly Gly
 225 230 235 240
 Leu Phe Asp Val Val Ser Thr Ala Leu Cys Ala Gly Ile Glu Asp Glu
 245 250 255
 Phe Thr Leu Asn Ala Val Met Gly Thr Trp Ala Val Thr Ser Gly Ile
 260 265 270
 Thr Arg Gly Leu Arg Asp Gly Glu Ala His Pro Tyr Val Tyr Gly Arg
 275 280 285
 Tyr Val Asn Asp Gly Glu Phe Ile Val His Glu Ala Ser Pro Thr Ser
 290 295 300
 Ser Gly Asn Leu Glu Trp Phe Thr Ala Gln Trp Gly Glu Ile Ser Phe
 305 310 315 320

Asp Glu Ile Asn Gln Ala Val Ala Ser Leu Pro Lys Ala Gly Gly Asp
 325 330 335
 Leu Phe Phe Leu Pro Phe Leu Tyr Gly Ser Asn Ala Gly Leu Glu Met
 340 345 350
 Thr Ser Gly Phe Tyr Gly Met Gln Ala Ile His Thr Arg Ala His Leu
 355 360 365
 Leu Gln Ala Ile Tyr Glu Gly Val Val Phe Ser His Met Thr His Leu
 370 375 380
 Asn Arg Met Arg Glu Arg Phe Thr Asp Val His Thr Leu Arg Val Thr
 385 390 395 400
 Gly Gly Pro Ala His Ser Asp Val Trp Met Gln Met Leu Ala Asp Val
 405 410 415
 Ser Gly Leu Arg Ile Glu Leu Pro Gln Val Glu Glu Thr Gly Cys Phe
 420 425 430
 Gly Ala Ala Leu Ala Ala Arg Val Gly Thr Gly Val Tyr His Asn Phe
 435 440 445
 Ser Glu Ala Gln Arg Asp Leu Arg His Pro Val Arg Thr Leu Leu Pro
 450 455 460
 Asp Met Thr Ala His Gln Leu Tyr Gln Lys Lys Tyr Gln Arg Tyr Gln
 465 470 475 480
 His Leu Ile Ala Ala Leu Gln Gly Phe His Ala Arg Ile Lys Glu His
 485 490 495

Thr Leu

<210> 27
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 <212> PRT
 <213> LyxK-Hi

<400> 27

Met His Tyr Tyr Leu Gly Ile Asp Cys Gly Gly Thr Phe Ile Lys Ala
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 Ala Ile Phe Asp Gln Asn Gly Thr Leu Gln Ser Ile Ala Arg Arg Asn
 20 25 30
 Ile Pro Ile Ile Ser Glu Lys Pro Gly Tyr Ala Glu Arg Asp Met Asp
 35 40 45
 Glu Leu Trp Asn Leu Cys Ala Gln Val Ile Gln Lys Thr Ile Arg Gln
 50 55 60

Ser Ser Ile Leu Pro Gln Gln Ile Lys Ala Ile Gly Ile Ser Ala Gln
 65 70 75 80
 Gly Lys Gly Ala Phe Phe Leu Asp Lys Asp Asn Lys Pro Leu Gly Arg
 85 90 95
 Ala Ile Leu Ser Ser Asp Gln Arg Ala Tyr Glu Ile Val Gln Cys Trp
 100 105 110
 Gln Lys Glu Asn Ile Leu Gln Lys Phe Tyr Pro Ile Thr Leu Gln Thr
 115 120 125
 Leu Trp Met Gly His Pro Val Ser Ile Leu Arg Trp Ile Lys Glu Asn
 130 135 140
 Glu Pro Ser Arg Tyr Glu Gln Ile His Thr Ile Leu Met Ser His Asp
 145 150 155 160
 Tyr Leu Arg Phe Cys Leu Thr Glu Lys Leu Tyr Cys Glu Glu Thr Asn
 165 170 175
 Ile Ser Glu Ser Asn Phe Tyr Asn Met Arg Glu Gly Lys Tyr Asp Ile
 180 185 190
 Gln Leu Ala Lys Leu Phe Gly Ile Thr Glu Cys Ile Asp Lys Leu Pro
 195 200 205
 Pro Ile Ile Lys Ser Asn Lys Ile Ala Gly Tyr Val Thr Ser Arg Ala
 210 215 220
 Ala Glu Gln Ser Gly Leu Val Glu Gly Ile Pro Val Val Gly Gly Leu
 225 230 235 240
 Phe Asp Val Val Ser Thr Ala Leu Cys Ala Asp Leu Lys Asp Asp Gln
 245 250 255
 His Leu Asn Val Val Leu Gly Thr Trp Ser Val Val Ser Gly Val Thr
 260 265 270
 His Tyr Ile Asp Asp Asn Gln Thr Ile Pro Phe Val Tyr Gly Lys Tyr
 275 280 285
 Pro Glu Lys Asn Lys Phe Ile Ile His Glu Ala Ser Pro Thr Ser Ala
 290 295 300
 Gly Asn Leu Glu Trp Phe Val Asn Gln Phe Asn Leu Pro Asn Tyr Asp
 305 310 315 320
 Asp Ile Asn His Glu Ile Ala Lys Leu Lys Pro Ala Ser Ser Ser Val
 325 330 335
 Leu Phe Ala Pro Phe Leu Tyr Gly Ser Asn Ala Lys Leu Gly Met Gln
 340 345 350
 Ala Gly Phe Tyr Gly Ile Gln Ser His His Thr Gln Ile His Leu Leu
 355 360 365

Gln Ala Ile Tyr Glu Gly Val Ile Phe Ser Leu Met Ser His Leu Glu
370 375 380

Arg Met Gln Val Arg Phe Pro Asn Ala Ser Thr Val Arg Val Thr Gly
385 390 395 400

Gly Pro Ala Lys Ser Glu Val Trp Met Gln Met Leu Ala Asp Ile Ser
405 410 415

Gly Met Arg Leu Glu Ile Pro Asn Ile Glu Glu Thr Gly Cys Leu Gly
420 425 430

Ala Ala Leu Met Ala Met Gln Ala Glu Ser Ala Val Glu Ile Ser Gln
435 440 445

Ile Leu Asn Ile Asp Arg Lys Ile Phe Leu Pro Asp Lys Asn Gln Tyr
450 455 460

Ser Lys Tyr Gln His Lys Tyr His Arg Tyr Leu Lys Phe Ile Glu Ala
465 470 475 480

Leu Lys Asn Leu Asp
485

<210> 28

<211> 220

<212> PRT

<213> YiaQ-Ec

<400> 28

Met Ser Arg Pro Leu Leu Gln Leu Ala Leu Asp His Ser Ser Leu Glu
1 5 10 15

Ala Ala Gln Arg Asp Val Thr Leu Leu Lys Asp Ser Val Asp Ile Val
20 25 30

Glu Ala Gly Thr Ile Leu Cys Leu Asn Glu Gly Leu Gly Ala Val Lys
35 40 45

Ala Leu Arg Glu Gln Cys Pro Asp Lys Ile Ile Val Ala Asp Trp Lys
50 55 60

Val Ala Asp Ala Gly Glu Thr Leu Ala Gln Gln Ala Phe Gly Ala Gly
65 70 75 80

Ala Asn Trp Met Thr Ile Ile Cys Ala Ala Pro Leu Ala Thr Val Glu
85 90 95

Lys Gly His Ala Met Ala Gln Arg Cys Gly Gly Glu Ile Gln Ile Glu
100 105 110

Leu Phe Gly Asn Trp Thr Leu Asp Asp Ala Arg Asp Trp His Arg Ile
115 120 125

Gly Val Arg Gln Ala Ile Tyr His Arg Gly Arg Asp Ala Gln Ala Ser
 130 135 140
 Gly Gln Gln Trp Gly Glu Ala Asp Leu Ala Arg Met Lys Ala Leu Ser
 145 150 155 160
 Asp Ile Gly Leu Glu Leu Ser Ile Thr Gly Gly Ile Thr Pro Ala Asp
 165 170 175
 Leu Pro Leu Phe Lys Asp Ile Arg Val Lys Ala Phe Ile Ala Gly Arg
 180 185 190
 Ala Leu Ala Gly Ala Ala Asn Pro Ala Gln Val Ala Gly Asp Phe His
 195 200 205
 Ala Gln Ile Asp Ala Ile Trp Gly Gly Ala Arg Ala
 210 215 220

<210> 29
 <211> 225
 <212> PRT
 <213> YiaQ-Hi

<400> 29

Met Gly Lys Pro Leu Leu Gln Ile Ala Leu Asp Ala Gln Tyr Leu Glu
 1 5 10 15
 Thr Ala Leu Val Asp Val Lys Gln Ile Glu His Asn Ile Asp Ile Ile
 20 25 30
 Glu Val Gly Thr Ile Leu Ala Cys Ser Glu Gly Met Arg Ala Val Arg
 35 40 45
 Ile Leu Arg Ala Leu Tyr Pro Asn Gln Ile Leu Val Cys Asp Leu Lys
 50 55 60
 Thr Thr Asp Ala Gly Ala Thr Leu Ala Lys Met Ala Phe Glu Ala Gly
 65 70 75 80
 Ala Asp Trp Leu Thr Val Ser Ala Ala Ala His Pro Ala Thr Lys Ala
 85 90 95
 Ala Cys Gln Lys Val Ala Glu Glu Phe Asn Lys Ile Gln Pro Asn Leu
 100 105 110
 Gly Val Pro Lys Glu Ile Gln Ile Glu Leu Tyr Gly Asn Trp Asn Phe
 115 120 125
 Asp Glu Val Lys Asn Trp Leu Gln Leu Gly Ile Lys Gln Ala Ile Tyr
 130 135 140
 His Arg Ser Arg Asp Ala Glu Leu Ser Gly Leu Ser Trp Ser Asn Gln
 145 150 155 160

Asp Ile Glu Asn Ile Glu Lys Leu Asp Ser Leu Gly Ile Glu Leu Ser
 165 170 175
 Ile Thr Gly Gly Ile Thr Pro Asp Asp Leu His Leu Phe Lys Asn Thr
 180 185 190
 Lys Asn Leu Lys Ala Phe Ile Ala Gly Arg Ala Leu Val Gly Lys Ser
 195 200 205
 Gly Arg Glu Ile Ala Glu Gln Leu Lys Gln Lys Ile Gly Gln Phe Trp
 210 215 220
 Ile
 225

<210> 30
 <211> 297
 <212> PRT
 <213> YiaR-Ec

<400> 30

Met Arg Lys Ser Thr Leu Ser Gly Glu Val Arg Val Arg Asn His Gln
 1 5 10 15
 Leu Gly Ile Tyr Glu Lys Ala Leu Ala Lys Asp Leu Ser Trp Pro Glu
 20 25 30
 Arg Leu Val Leu Ala Lys Ser Cys Gly Phe Asp Phe Val Glu Met Ser
 35 40 45
 Val Asp Glu Thr Asp Glu Arg Leu Ser Arg Leu Asp Trp Ser Ala Ala
 50 55 60
 Gln Arg Thr Ser Leu Val Ala Ala Met Ile Glu Thr Gly Val Gly Ile
 65 70 75 80
 Pro Ser Met Cys Leu Ser Ala His Arg Arg Phe Pro Phe Gly Ser Arg
 85 90 95
 Asp Glu Ala Val Arg Glu Arg Ala Arg Glu Ile Met Ser Lys Ala Ile
 100 105 110
 Arg Leu Ala Arg Asp Leu Gly Ile Arg Thr Ile Gln Leu Ala Gly Tyr
 115 120 125
 Asp Val Tyr Tyr Glu Asp His Asp Glu Gly Thr Arg Gln Arg Phe Ala
 130 135 140
 Glu Gly Leu Ala Trp Ala Val Glu Gln Ala Ala Ala Ser Gln Val Met
 145 150 155 160
 Leu Ala Val Glu Ile Met Asp Thr Ala Phe Met Asn Ser Ile Ser Lys
 165 170 175

Trp Lys Lys Trp Asp Glu Met Leu Ala Ser Pro Trp Phe Thr Val Tyr
 180 185 190
 Pro Asp Val Gly Asn Leu Ser Ala Trp Gly Asn Asp Val Pro Ala Glu
 195 200 205
 Leu Lys Leu Gly Ile Asp Arg Ile Ala Ala Ile His Leu Lys Asp Thr
 210 215 220
 Gln Pro Val Thr Gly Gln Ser Pro Gly Gln Phe Arg Asp Val Pro Phe
 225 230 235 240
 Gly Glu Gly Cys Val Asp Phe Val Gly Ile Phe Lys Thr Leu His Lys
 245 250 255
 Leu Asn Tyr Arg Gly Ser Phe Leu Ile Glu Met Trp Thr Glu Lys Ala
 260 265 270
 Lys Glu Pro Val Leu Glu Ile Ile Gln Ala Arg Arg Trp Ile Glu Ala
 275 280 285
 Arg Met Gln Glu Ala Gly Phe Ile Cys
 290 295

<210> 31
 <211> 286
 <212> PRT
 <213> YiaR-Hi

<400> 31

Met Lys Lys His Lys Ile Gly Ile Tyr Glu Lys Ala Leu Pro Lys Asn
 1 5 10 15
 Ile Thr Trp Gln Glu Arg Leu Ser Leu Ala Lys Ala Cys Gly Phe Glu
 20 25 30
 Phe Ile Glu Met Ser Ile Asp Glu Ser Asn Asp Arg Leu Ser Arg Leu
 35 40 45
 Asn Trp Thr Lys Ser Glu Arg Ile Ala Leu His Gln Ser Ile Ile Gln
 50 55 60
 Ser Gly Ile Thr Ile Pro Ser Met Cys Leu Ser Ala His Arg Arg Phe
 65 70 75 80
 Pro Phe Gly Ser Lys Asp Lys Lys Ile Arg Gln Lys Ser Phe Glu Ile
 85 90 95
 Met Glu Lys Ala Ile Asp Leu Ser Val Asn Leu Gly Ile Arg Thr Ile
 100 105 110
 Gln Leu Ala Gly Tyr Asp Val Tyr Tyr Glu Lys Gln Asp Glu Glu Thr
 115 120 125

Ile Lys Tyr Phe Gln Glu Gly Ile Glu Phe Ala Val Thr Leu Ala Ala
130 135 140

Ser Ala Gln Val Thr Leu Ala Val Glu Ile Met Asp Thr Pro Phe Met
145 150 155 160

Ser Ser Ile Ser Arg Trp Lys Lys Trp Asp Thr Ile Ile Asn Ser Pro
165 170 175

Trp Phe Thr Val Tyr Pro Asp Ile Gly Asn Leu Ser Ala Trp Asn Asn
180 185 190

Asn Ile Glu Glu Glu Leu Thr Leu Gly Ile Asp Lys Ile Ser Ala Ile
195 200 205

His Leu Lys Asp Thr Tyr Pro Val Thr Glu Thr Ser Lys Gly Gln Phe
210 215 220

Arg Asp Val Pro Phe Gly Gln Gly Cys Val Asp Phe Val His Phe Phe
225 230 235 240

Ser Leu Leu Lys Lys Leu Asn Tyr Arg Gly Ala Phe Leu Ile Glu Met
245 250 255

Trp Thr Glu Lys Asn Glu Glu Pro Leu Leu Glu Ile Ile Gln Ala Arg
260 265 270

Lys Trp Ile Val Gln Gln Met Glu Lys Ala Gly Leu Leu Cys
275 280 285

<210> 32

<211> 231

<212> PRT

<213> YiaS-Ec

<400> 32

Met Leu Glu Gln Leu Lys Ala Asp Val Leu Ala Ala Asn Leu Ala Leu
1 5 10 15

Pro Ala His His Leu Val Thr Phe Thr Trp Gly Asn Val Ser Ala Val
20 25 30

Asp Glu Thr Arg Gln Trp Met Val Ile Lys Pro Ser Gly Val Glu Tyr
35 40 45

Asp Val Met Thr Ala Asp Asp Met Val Val Val Glu Ile Ala Ser Gly
50 55 60

Lys Val Val Glu Gly Ser Lys Lys Pro Ser Ser Asp Thr Pro Thr His
65 70 75 80

Leu Ala Leu Tyr Arg Arg Tyr Ala Glu Ile Gly Gly Ile Val His Thr
85 90 95

His Ser Arg His Ala Thr Ile Trp Ser Gln Ala Gly Leu Asp Leu Pro
 100 105 110
 Ala Trp Gly Thr Thr His Ala Asp Tyr Phe Tyr Gly Ala Ile Pro Cys
 115 120 125
 Thr Arg Gln Met Thr Ala Glu Glu Ile Asn Gly Glu Tyr Glu Tyr Gln
 130 135 140
 Thr Gly Glu Val Ile Ile Glu Thr Phe Glu Glu Arg Gly Arg Ser Pro
 145 150 155 160
 Ala Gln Ile Pro Ala Val Leu Val His Ser His Gly Pro Phe Ala Trp
 165 170 175
 Gly Lys Asn Ala Ala Asp Ala Val His Asn Ala Val Val Leu Glu Glu
 180 185 190
 Cys Ala Tyr Met Gly Leu Phe Ser Arg Gln Leu Ala Pro Gln Leu Pro
 195 200 205
 Ala Met Gln Asn Glu Leu Leu Asp Lys His Tyr Leu Arg Lys His Gly
 210 215 220
 Ala Asn Ala Tyr Tyr Gly Gln
 225 230

<210> 33
 <211> 231
 <212> PRT
 <213> YiaS-Hi

<400> 33

Met Leu Ala Gln Leu Lys Lys Glu Val Phe Glu Ala Asn Leu Ala Leu
 1 5 10 15
 Pro Lys His His Leu Val Thr Phe Thr Trp Gly Asn Val Ser Ala Ile
 20 25 30
 Asp Arg Glu Lys Asn Leu Val Val Ile Lys Pro Ser Gly Val Asp Tyr
 35 40 45
 Asp Val Met Thr Glu Asn Asp Met Val Val Val Asp Leu Phe Thr Gly
 50 55 60
 Asn Ile Val Glu Gly Asn Lys Lys Pro Ser Ser Asp Thr Pro Thr His
 65 70 75 80
 Leu Glu Leu Tyr Arg Gln Phe Pro His Ile Gly Gly Ile Val His Thr
 85 90 95
 His Ser Arg His Ala Thr Ile Trp Ala Gln Ala Gly Leu Asp Ile Ile
 100 105 110

[illegible]

DECLARATION AND POWER OF ATTORNEY
Utility Application

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled **METABOLIC SELECTION METHODS** the specification of which

(Check One)



is attached hereto OR



was filed on _____ as United States Application Serial No. _____ or PCT International Application No. _____ and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment(s) referred to above.

I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with Title 37, Code of Federal Regulations, § 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or of any PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application Number(s)	Country	Date of Filing	Priority Claimed	
			Yes	No

I hereby claim the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below.

Application Number(s)	Filing Date

I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s), or § 365(c) of any PCT international application designating the United States of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

U.S. Parent Application Number	PCT Parent Number	Parent Filing Date	Status-Patented, Pending or Abandoned

POWER OF ATTORNEY: As a named inventor, I hereby appoint as my attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith:

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Send Correspondence to: Richard J. Warburg	LYON & LYON LLP 633 W Fifth St., Suite 4700 Los Angeles, CA 90071	Direct Telephone calls to: Richard J. Warburg
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Residence, post office address, citizenship and signature of inventor(s) set forth beginning on next page.

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	FULL NAME OF INVENTOR	FIRST Name Veronique	MIDDLE Initial	LAST Name Dartois	
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203	RESIDENCE & CITIZENSHIP	City	State or Foreign Country	Country of Citizenship	
	POST OFFICE ADDRESS		City	State or Country	Zip Code
	FULL NAME OF INVENTOR	FIRST Name	MIDDLE Initial	LAST Name	
204	RESIDENCE & CITIZENSHIP	City	State or Foreign Country	Country of Citizenship	
	POST OFFICE ADDRESS		City	State or Country	Zip Code
	FULL NAME OF INVENTOR	FIRST Name	MIDDLE Initial	LAST Name	
205	RESIDENCE & CITIZENSHIP	City	State or Foreign Country	Country of Citizenship	
	POST OFFICE ADDRESS		City	State or Country	Zip Code
	FULL NAME OF INVENTOR	FIRST Name	MIDDLE Initial	LAST Name	
206	RESIDENCE & CITIZENSHIP	City	State or Foreign Country	Country of Citizenship	
	POST OFFICE ADDRESS		City	State or Country	Zip Code

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Title 18, United States Code §1001, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Signature of Inventor	201
Date	10-12-98
Signature of Inventor	202
Date	10-10-98
Signature of Inventor	203
Date	

Signature of Inventor	204
Date	
Signature of Inventor	205
Date	
Signature of Inventor	206
Date	

(Signatures should conform to names as presented at 201 et seq. above.)